Structure of everninomicin (Ziracin)

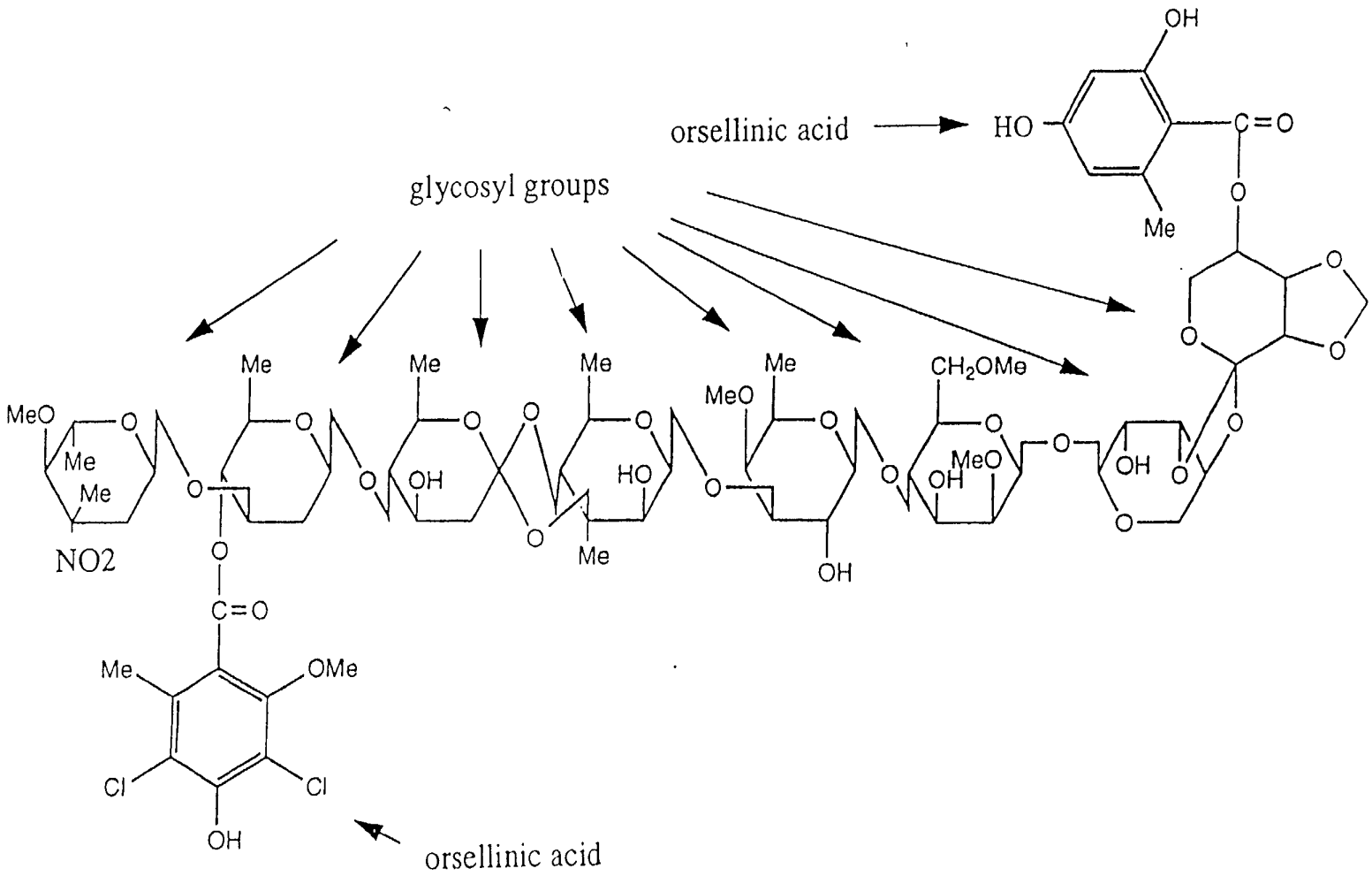


Figure 1

Overlapping cosmids and clones spanning 185 kb of chromosomal DNA containing the Everninomicin Pathway region.

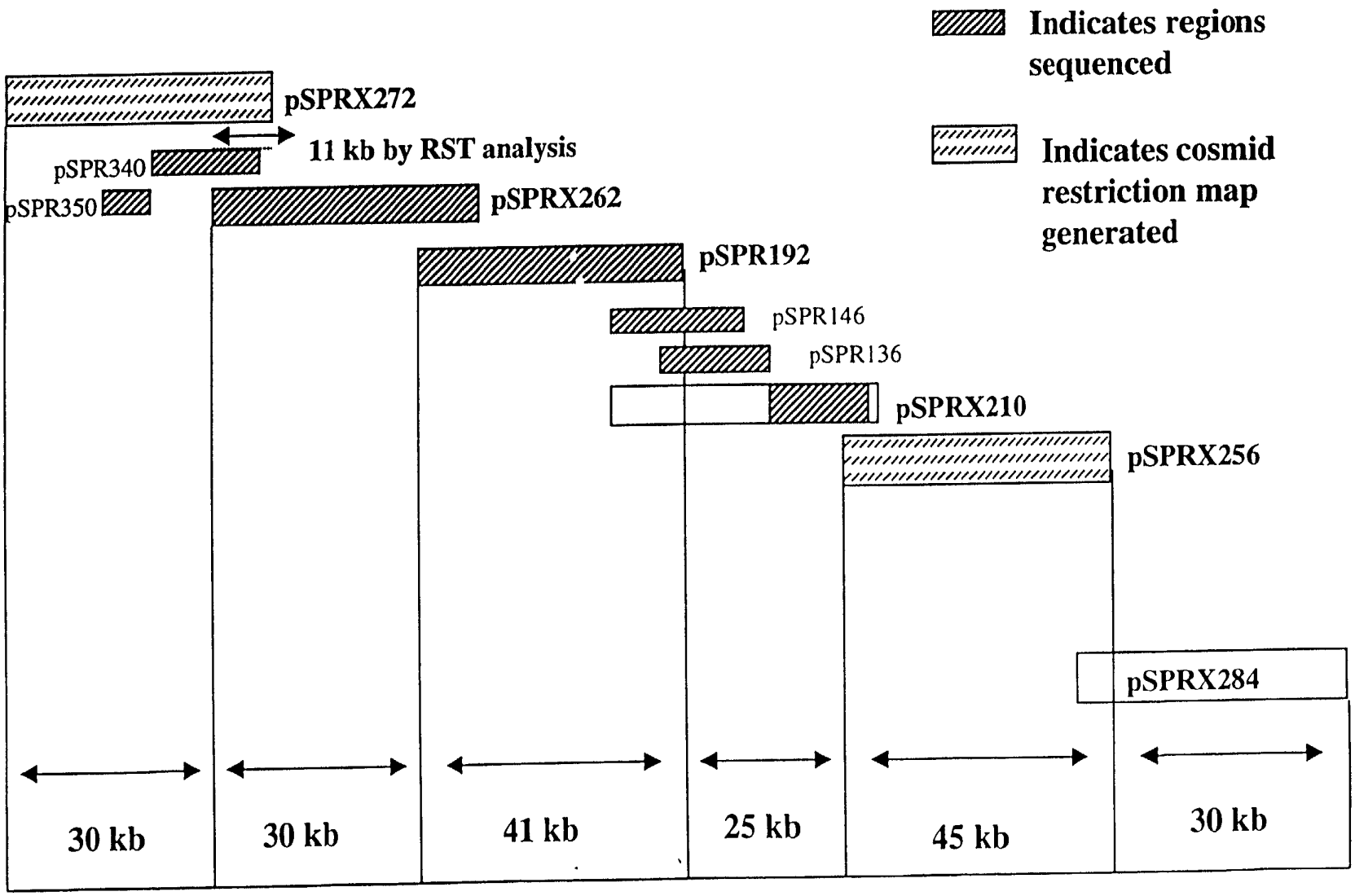


Figure 2A

pSPRX272
37.5kb

Cosmid pSPRX272

Regions sequenced indicated by crosshatches.

Fragments cloned indicated by clone designation benigth fragment.

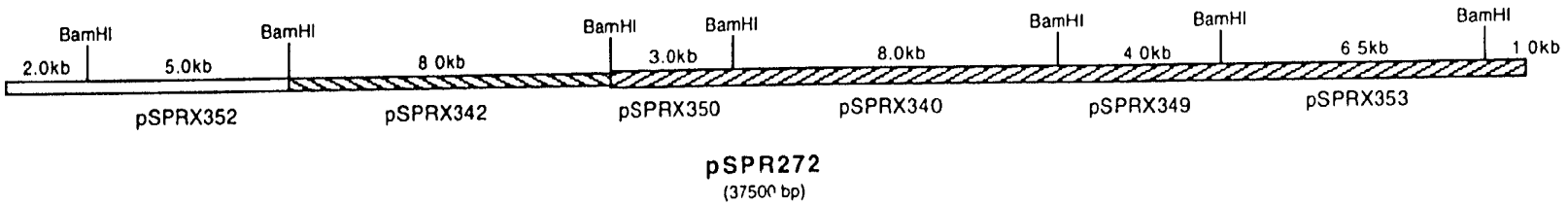


Figure 2B

Cosmid pSPRX256

Regions sequenced indicated by crosshatches.

Fragments cloned indicated by clone designation benigth fragment.

Cosmid
pSPRX256

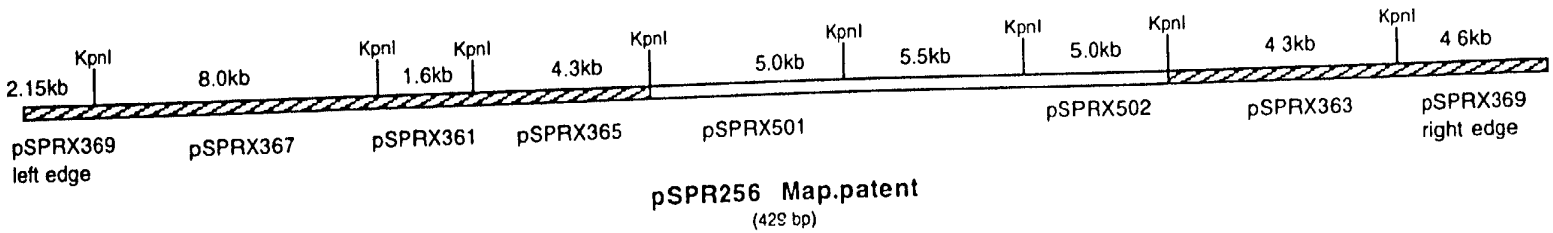
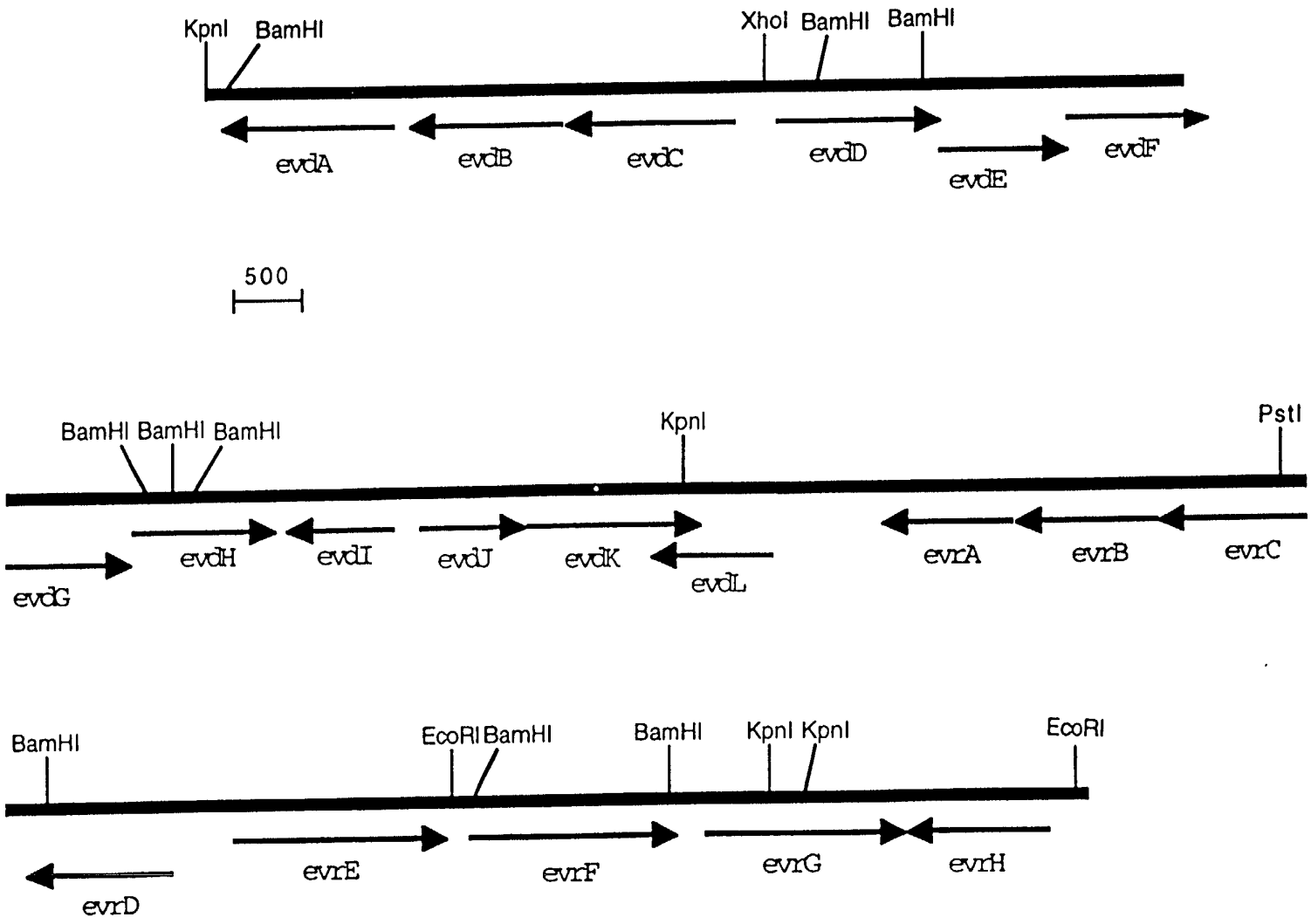


Figure 2C

Figure 3 (A)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XhoI
BamHI
BamHI
evdA
evdB
evdC
evdD
evdE
evdF
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BamHI
KpnI
PstI
evdG
evdH
evdI
evdJ
evdK
evdL
evrA
evrB
evrC
BamHI
EcoRI
BamHI
BamHI
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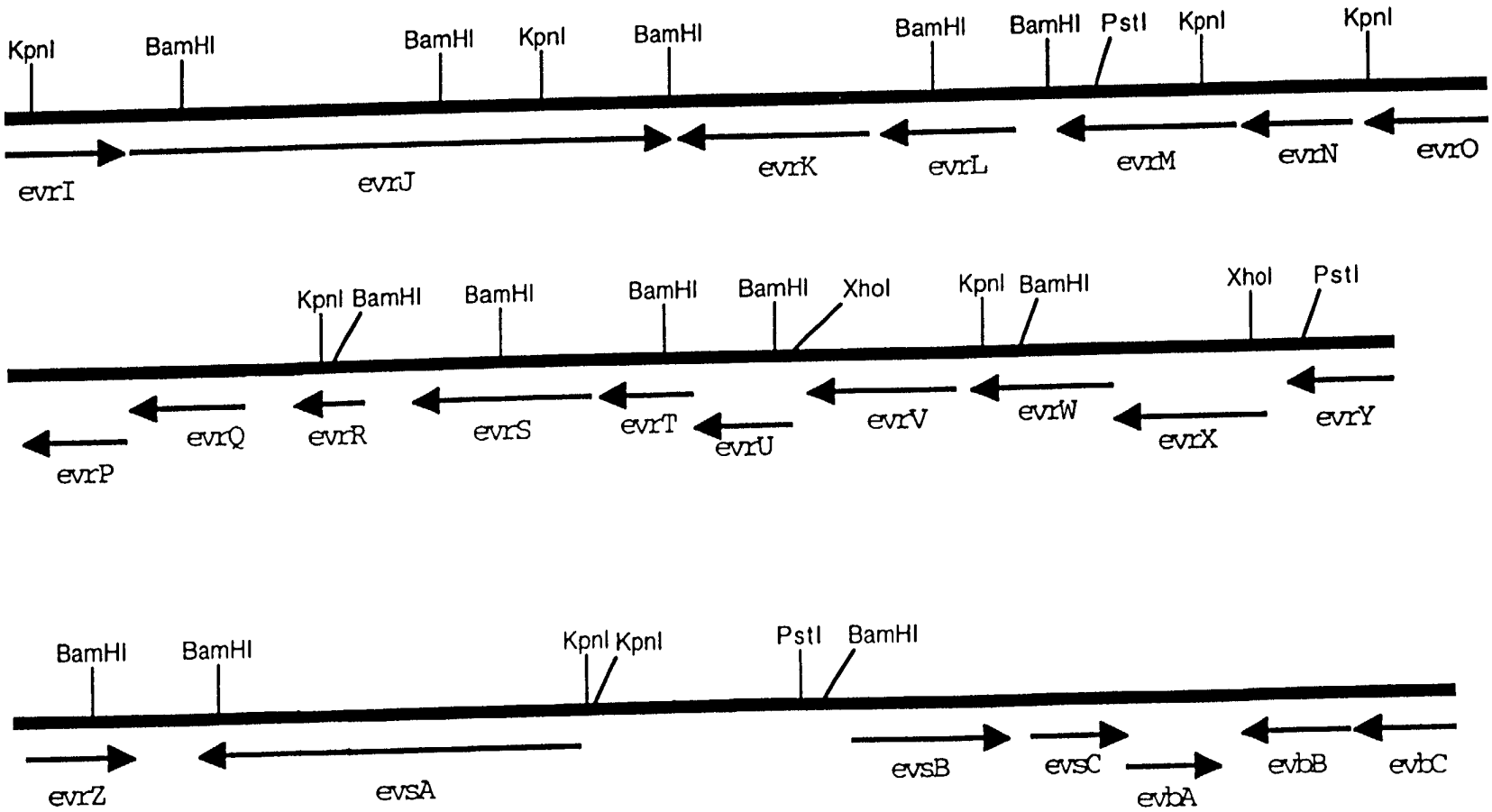
evrD
evrE
evrF
evrG
evrH

Figure 3 (B)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KpnI
BamHI
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KpnI
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evrL
evrM
evrN
evrO
KpnI
BamHI
BamHI
BamHI
BamHI
XhoI
KpnI
BamHI
XhoI
PstI
evrP
evrQ
evrR
evrS
evrT
evrU
evrV
evrW
evrX
evrY
BamHI
BamHI
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KpnI
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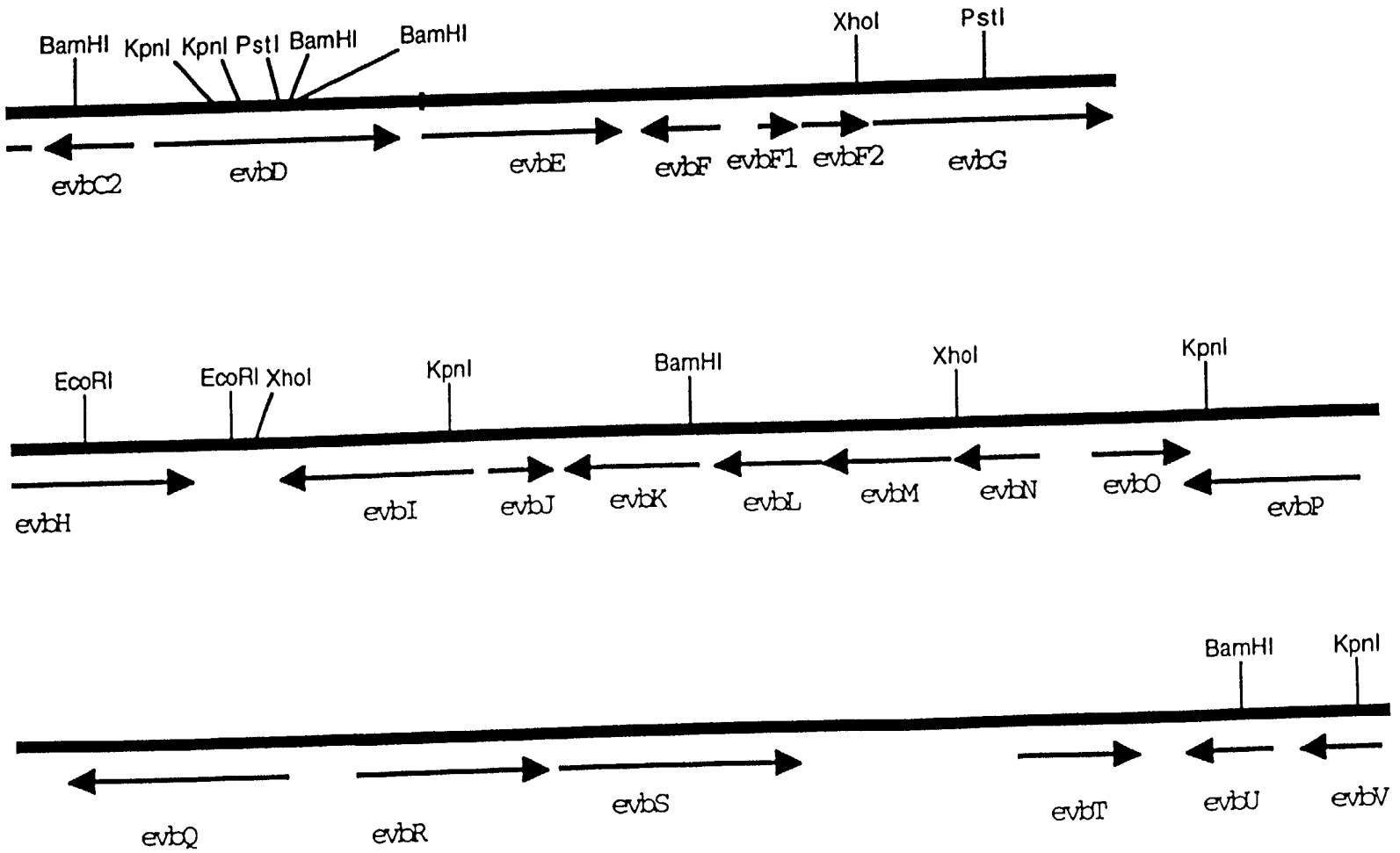
BamHI
evrZ
evsA
evsB
evsC
evbA
evbB
evbC

Figure 3 (C)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evbF2
evbG
EcoRI
EcoRI
XhoI
KpnI
BamHI
XhoI
KpnI
evbH
evbI
evbJ
evbK
evbL
evbM
evbN
evbO
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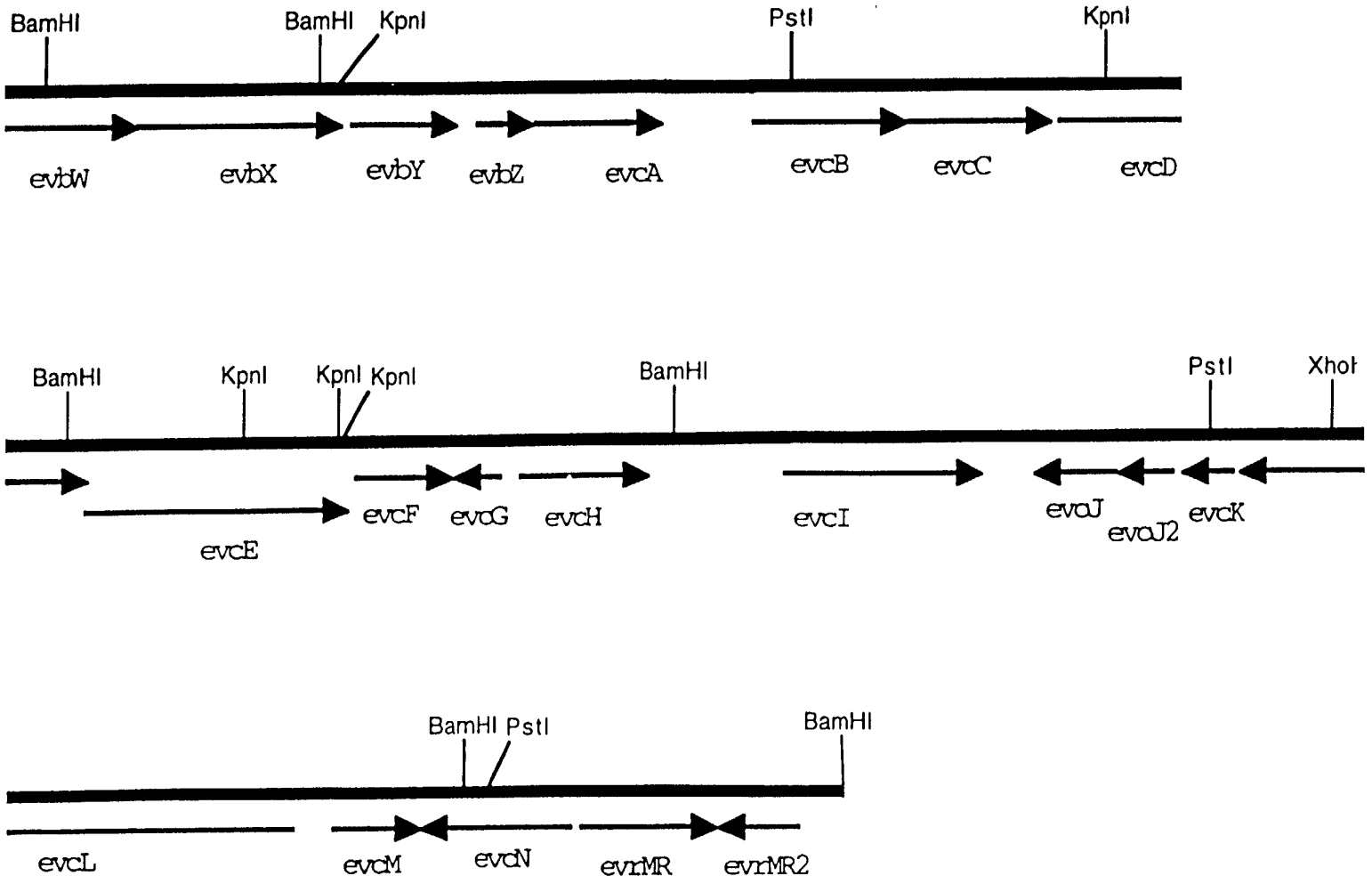
evbQ
evbR
evbS
evbT
evbU
evbV

Figure 3 (D)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KpnI
KpnI
KpnI
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XhoI
evcE
evcF
evcG
evcH
evcI
evcJ
evcJ2
evcK
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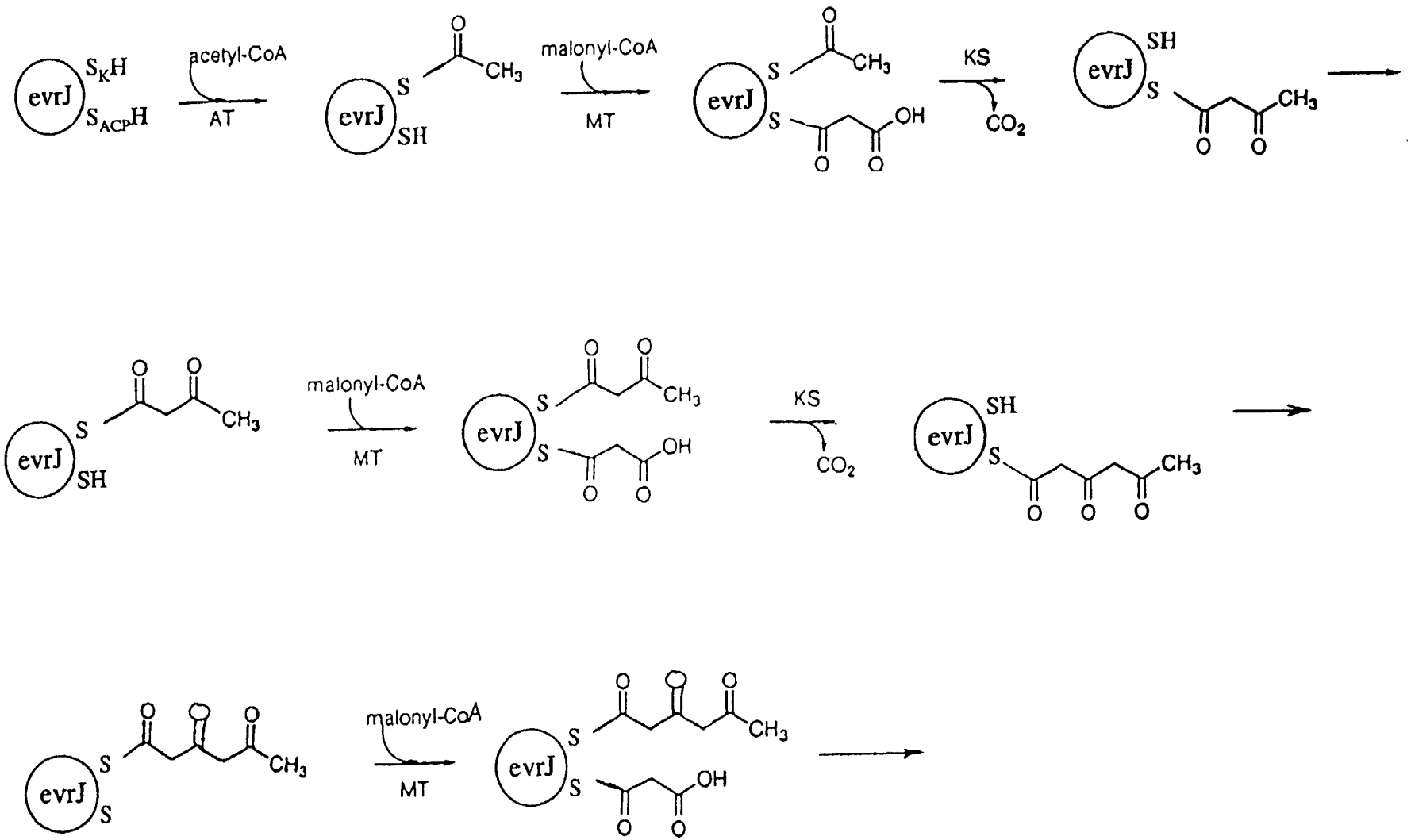
evcN
evrMR
evrMR2

EP 1 778 860 B1

Figure 4 (A)



EP 1 750 769 A2

Figure 4 (B)

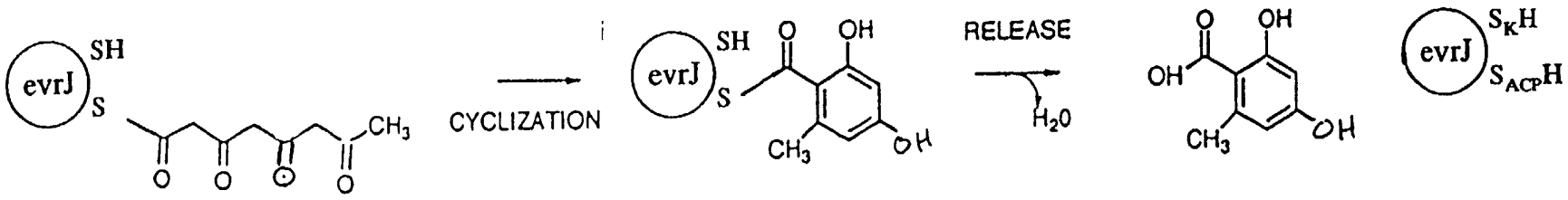
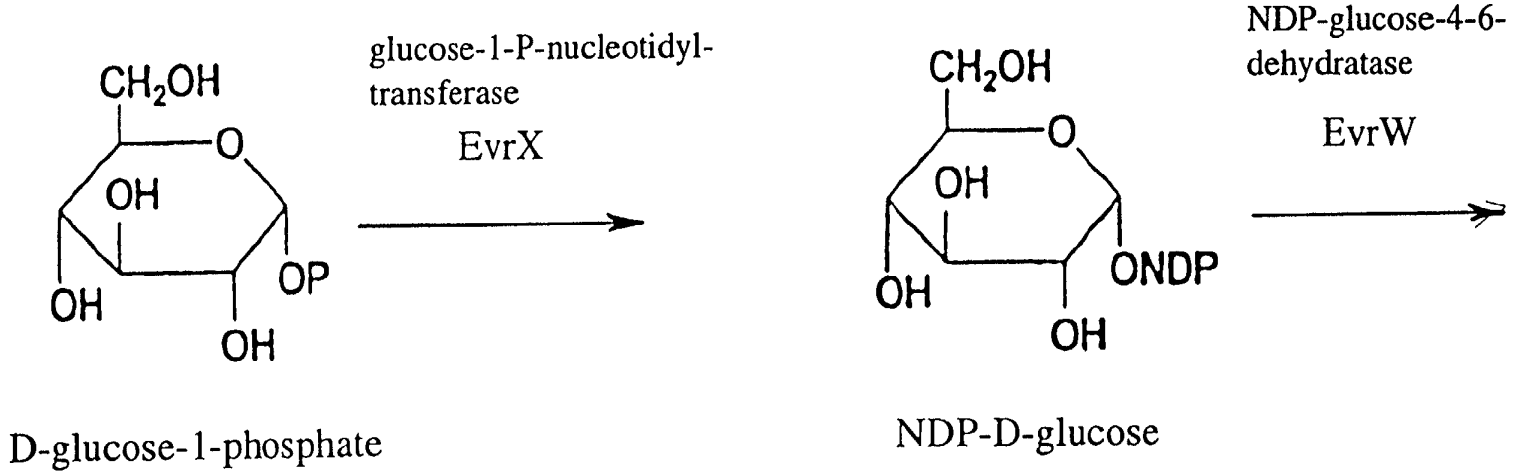


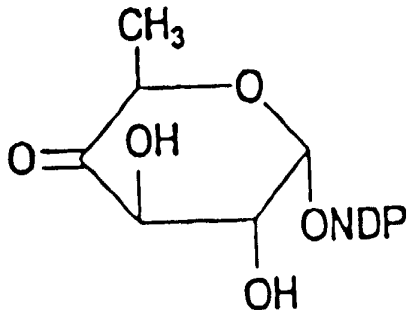
Figure 5 (A)



D-glucose-1-phosphate

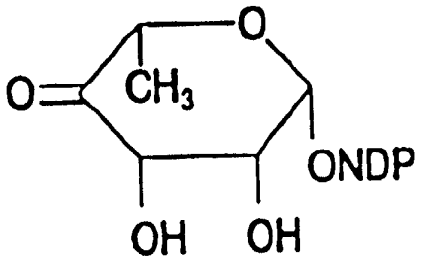
NDP-D-glucose

Figure 5 (B)



NDP-4-keto-6-deoxyglucos
3,5 epimerase

EvrV



NDP-4-keto-6-deoxy-
D-glucose

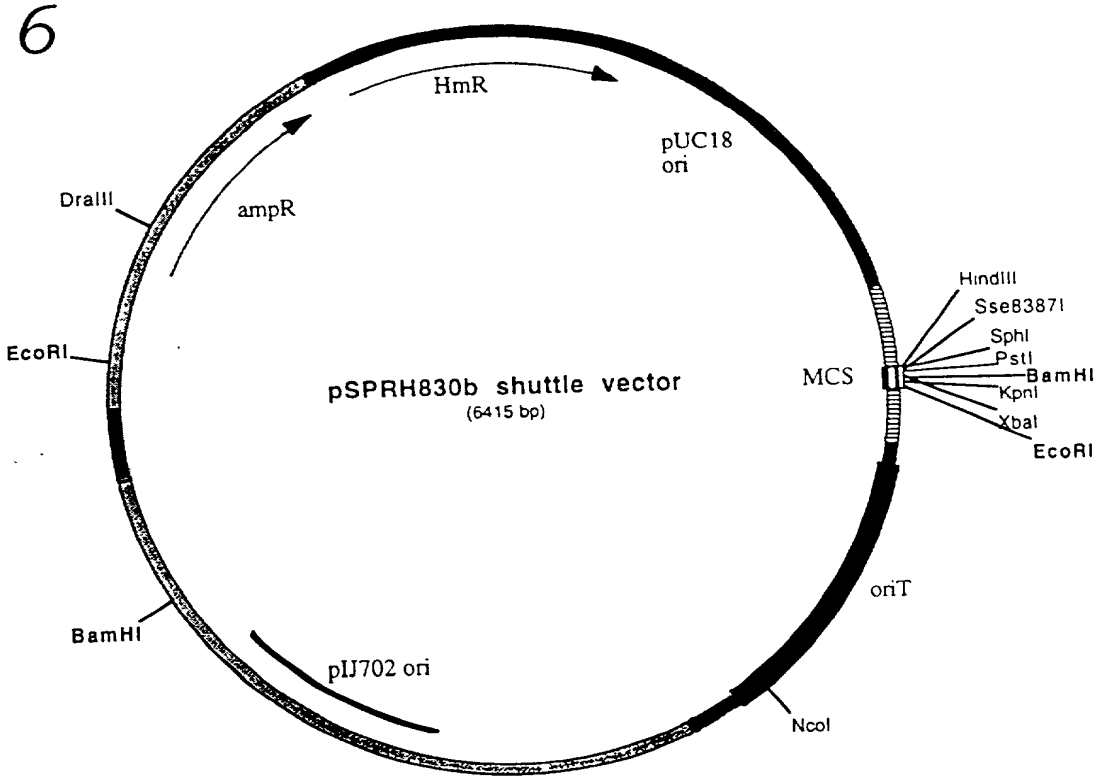
↓ Modifications and
↓ Glycosyltransferase
↓ attachment
to Everninomicin

NDP-4-keto-rhamnose

↓
↓
↓

pSPRH830b *E.coli*-Micromonospora shuttle vector

Figure 6



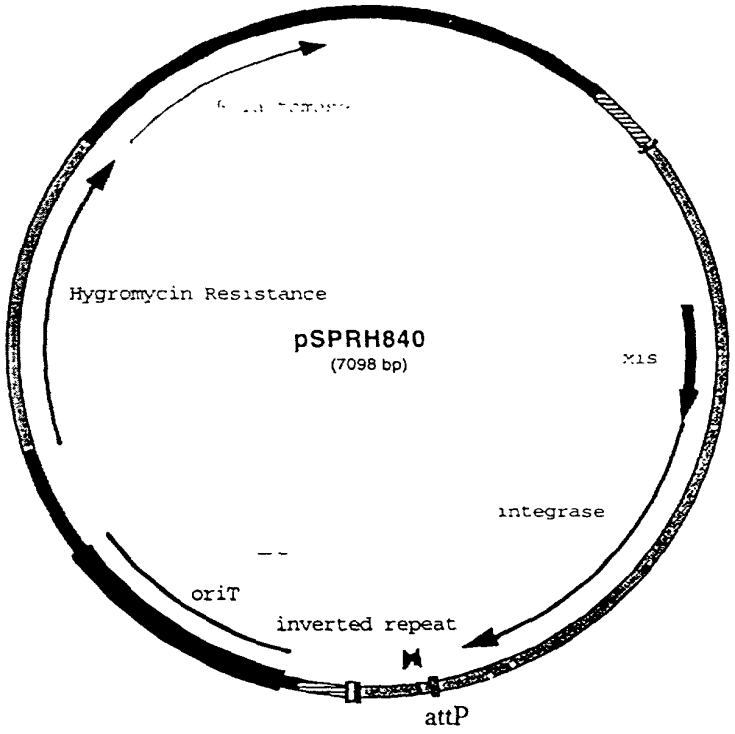
pSPRH830b - pSPRH826b backbone

Function	Source
- Ampicillin resistance	(pUC18)
- Multiple cloning site	(pUC18)
- pUC18 origin	(pUC18)
- Hygromycin resistance	(p16R1)
- oriT (origin of transfer)	(pRL1058)
- pIJ702 origin of replication	(pIJ702)

09/958,756 - 371 Date: 10/4/01

pSPRH840 integrating vector

Figure 7A



pSPRH840 - pSPRH826b backbone, pMLP1 *xis, int* attP insert

pSPRH840 conjugated from *E. coli* into	HmR transformants obtained
M.carbonacea	+
M.rosaria	-
M.halophitica	+

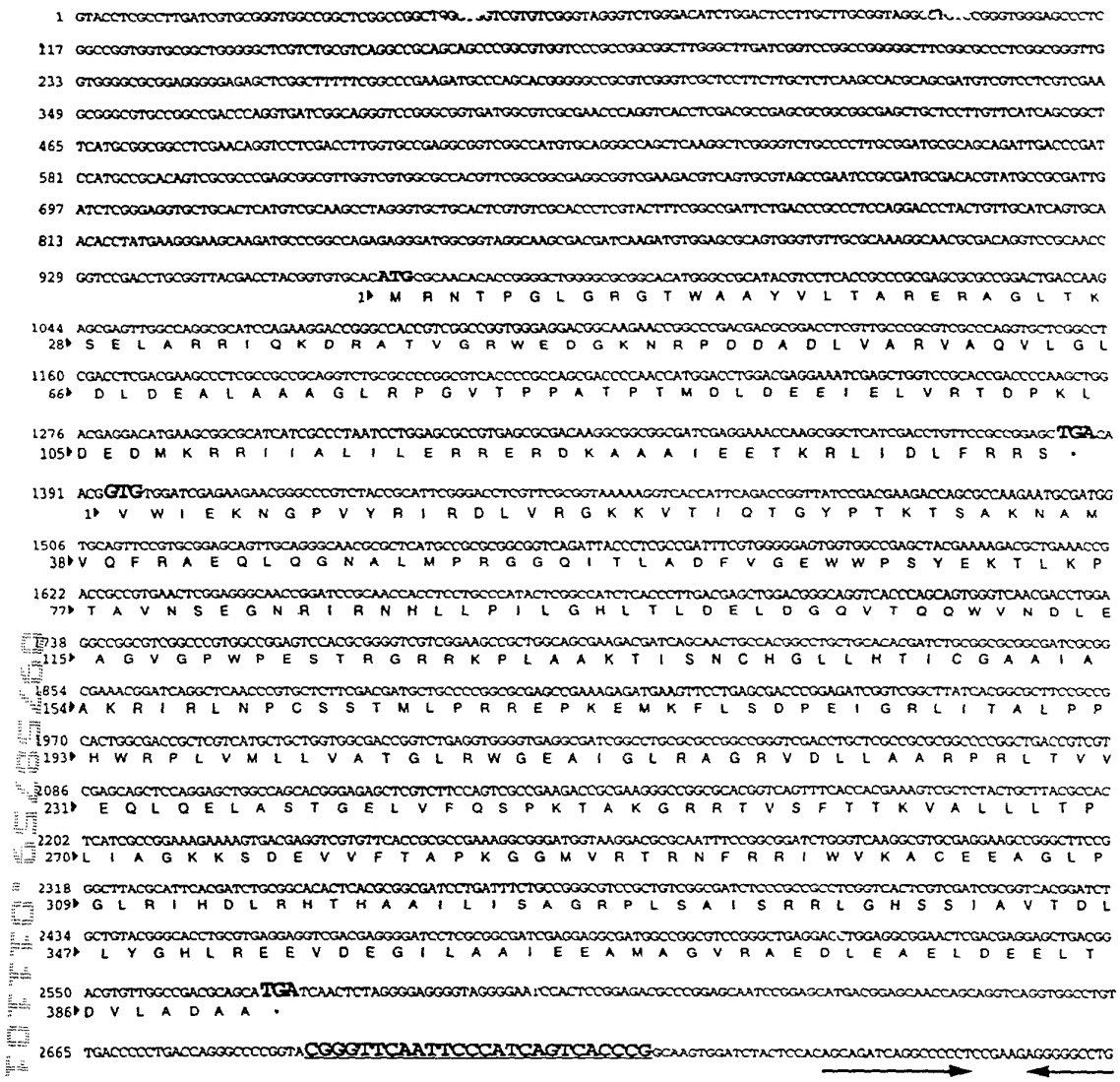


Figure 7B

pSPRH826b Insertion plasmid

Figure 8

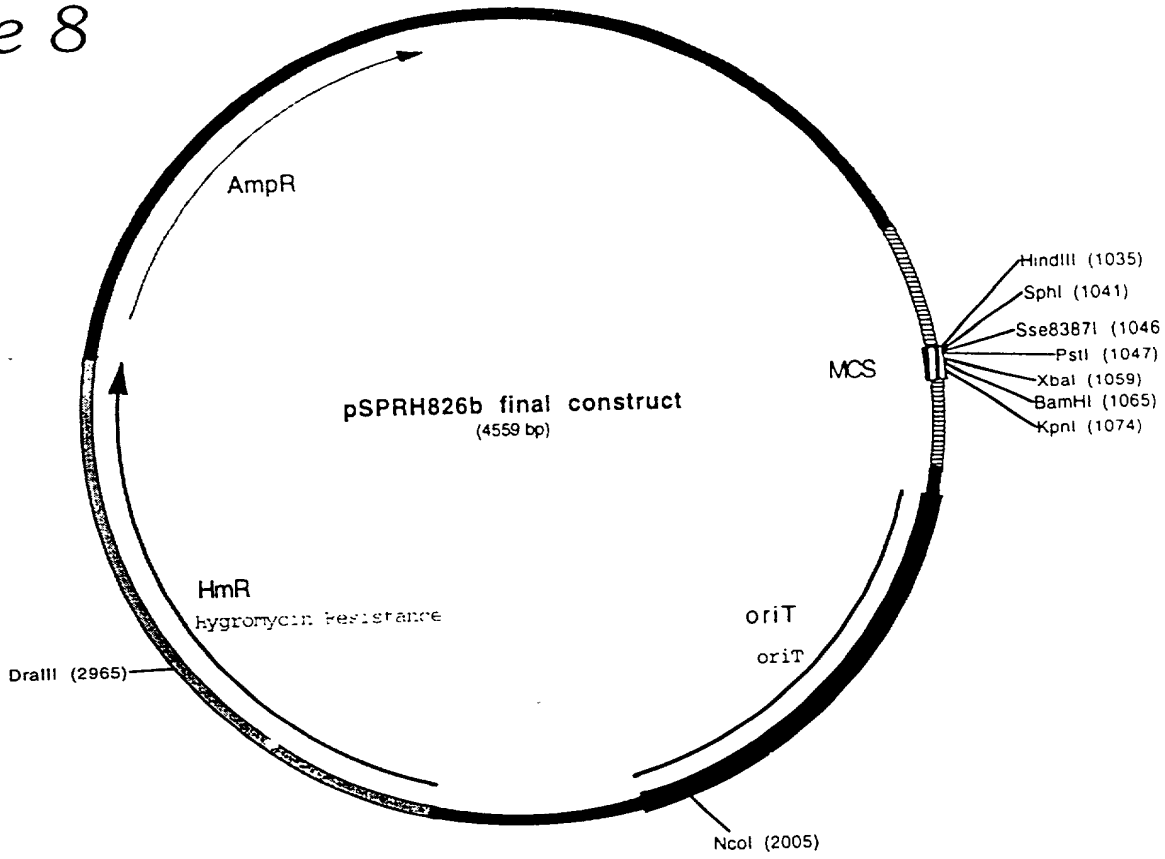


Figure 9

Analysis of *M. carbonacea* and *M. halophytica* pSPRH840 insertion site AttB/AttP region

A. Alignment of pMLP1 attP region with religation clone edge sequence

```
M.halophytica PstI relig-9   TGATCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCGGAGACGCCCGGAGCAATCCGGA  60
M.carb PstI relig-1          TGATCAACTCTAGGGGAGGGGTAGGGGAAT-CNCTCCGGAGACGCCCGGAGCAATCCGGA  59
M.carb PstI relig-4          TGATCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCGGAGACGCCCGGAGCAATCCGGA  60
pMLP1.intTGA.att region      TGATCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCGGAGACGCCCGGAGCAATCCGGA  60
Consensus                    TGATCAACTCTAGGGGAGGGGTAGGGGAATCCNCTCCGGAGACGCCCGGAGCAATCCGGA  60

M.halophytica PstI relig-9   GCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCAGGGCCCCGGTA  120
M.carb PstI relig-1          GCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCAGGGCCCCGGTA  119
M carb PstI relig-4          GCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCAGGGCCCCGGTA  120
pMLP1 intTGA.att region      GCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCAGGGCCCCGGTA  120
Consensus                    GCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCAGGGCCCCGGTA  120

M halophytica PstI relig-9   CGGGTTCAATTCCCATCAGTCACCCCAGGTAAGACCCAGGTCAGGGCCGGTTCTCACC-G  179
M carb PstI relig-1          CGGGTTCAATTCCCATCAGTCACCC---GT-ACACGAAGGCCCCCTCCAC-TCGGAGGGG  174
M carb PstI relig-4          CGGGTTCAATTCCCATCAGTCACCC---GT-ACACGAAGGCCCCCTCCAC-TCGGAGGGG  175
pMLP1 intTGA.att region      CGGGTTCAATTCCCATCAGTCACCC---G--GCAAGTGGATCTACTCCACAGCAGATCAG  175
Consensus                    CGGGTTCAATTCCCATCAGTCACCCCAGGTARSAMSHRGRYCHVSKCCRSWKCDSABSRG  180

M halophytica PstI relig-9   GCCCT-GACGCATTTTCAGGGG-------                               200
M.carb PstI relig-1          GCCTTCGGCGT-TCCTGAGGGTTCCCG-                               200
M.carb PstI relig-4          GCCTTCGGCGT-TCCTGAGGGTTCGC---                              200
pMLP1.intTGA.att region      GCCCCCTCCG----AAGAGGGGGCCTGAT                              209
Consensus                    GCCYYCKVCGYATYHWSAGGGKKCSYGAT
```

Insertion juncture

B. pMLP1 attP region

```
1   TGATCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCGGAGACGCCCGGAGCAATCCGGAGCAATGACGGAGCAACCAGCAGGTCAGGTGGCCT

94  GTTGACCCCCTGACCAGGGCCCCGGTACGGGTTCAATTCCCATCAGTCACCCCGGCAAGTGGATCTACTCCACAGCAGATC

174 AGGCCCCCTCCGAAGAGGGGGCCTGATGCGTCATAGGGGACAGGTAGGGGAACTCAA
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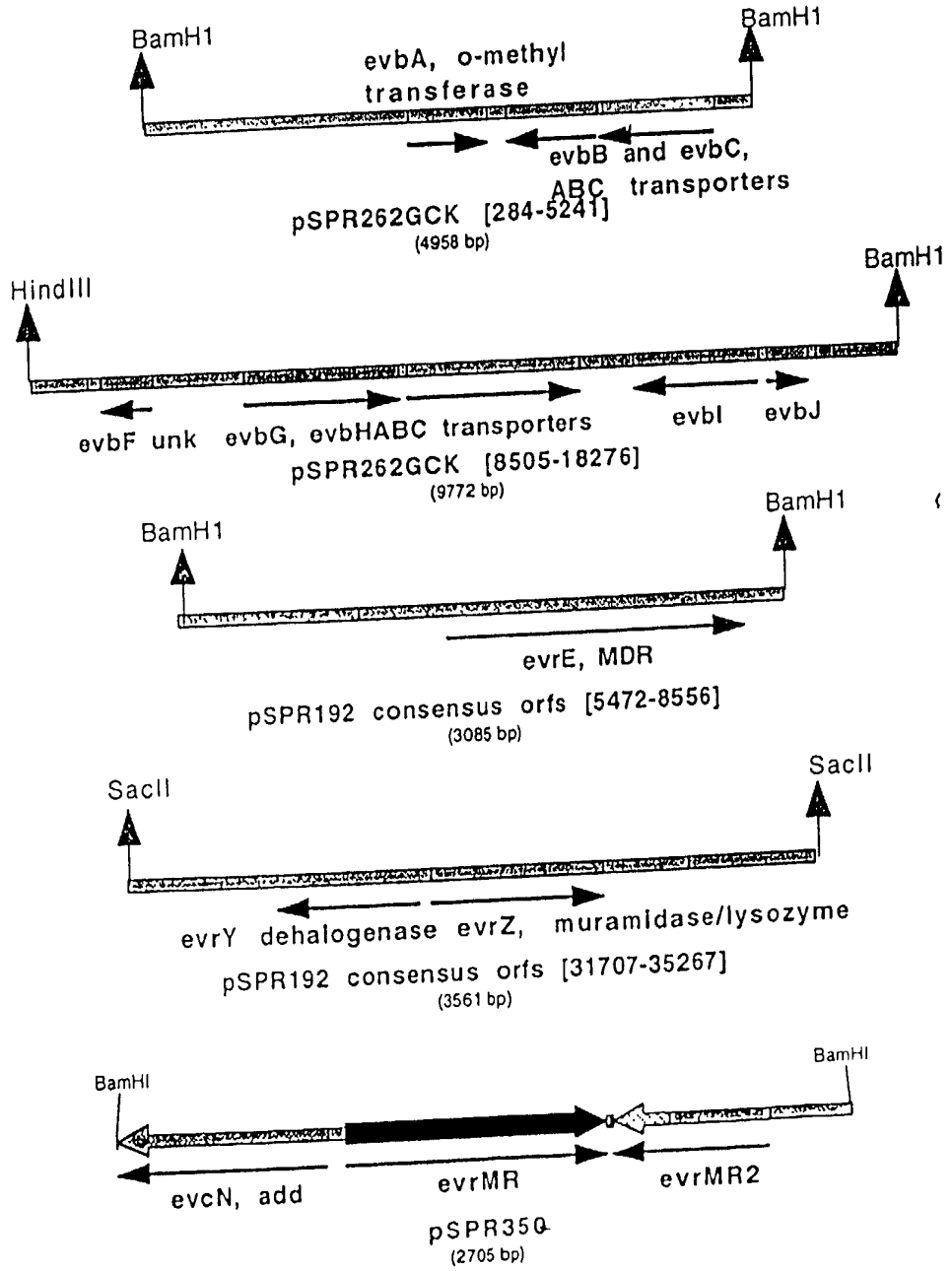
Figure 10

Cloning scheme to test potential resistance genes



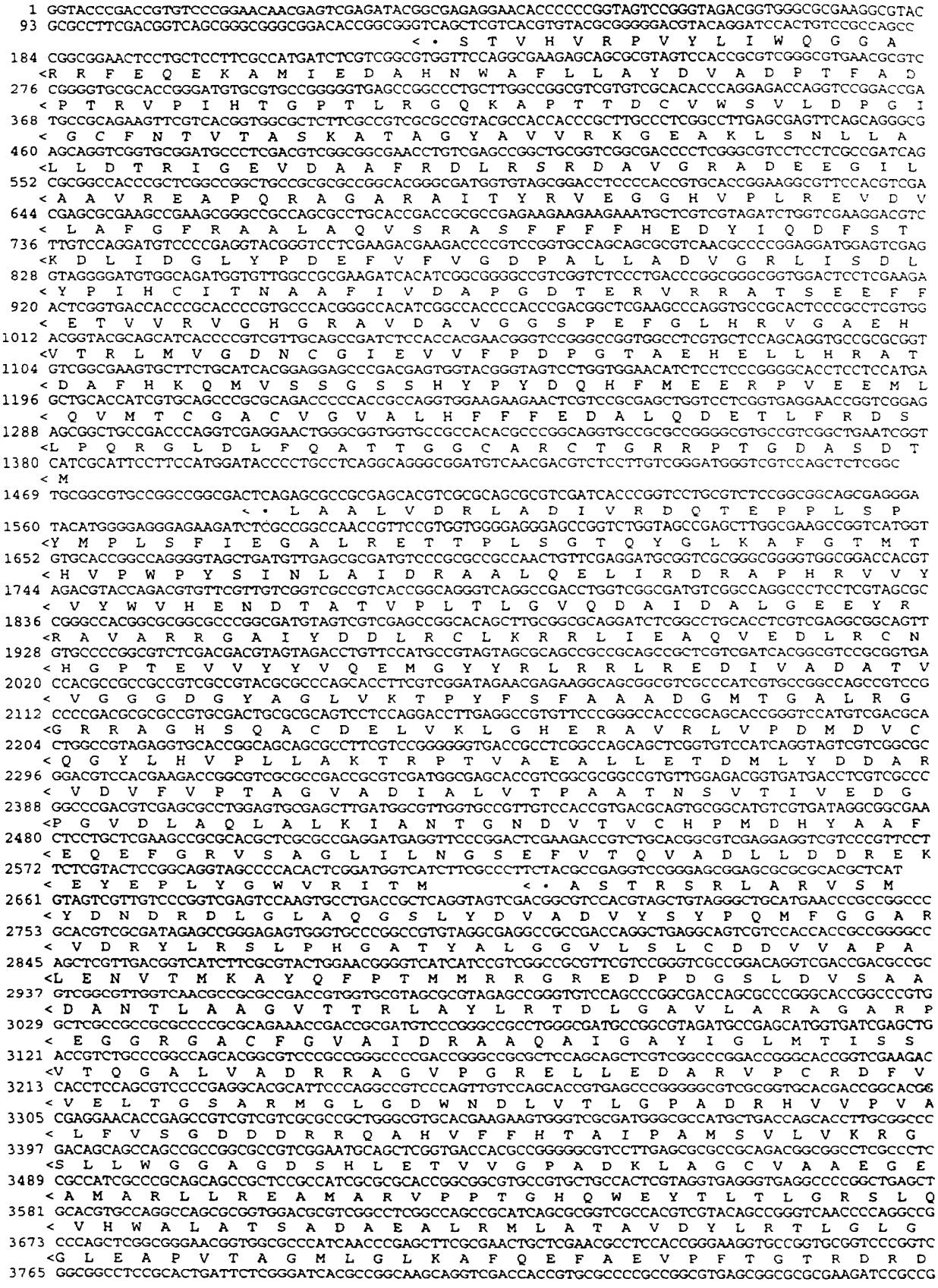


Figure 11A

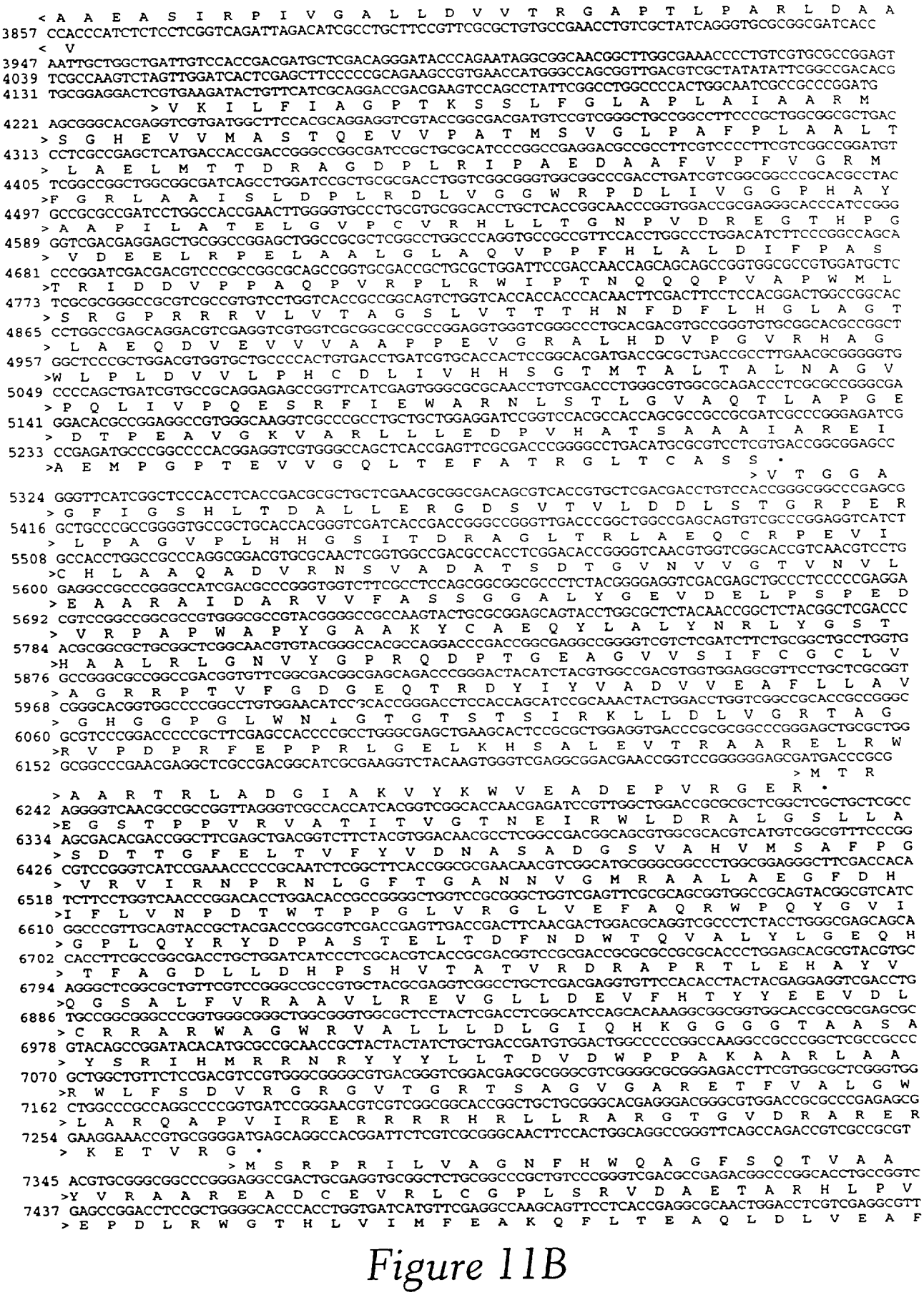
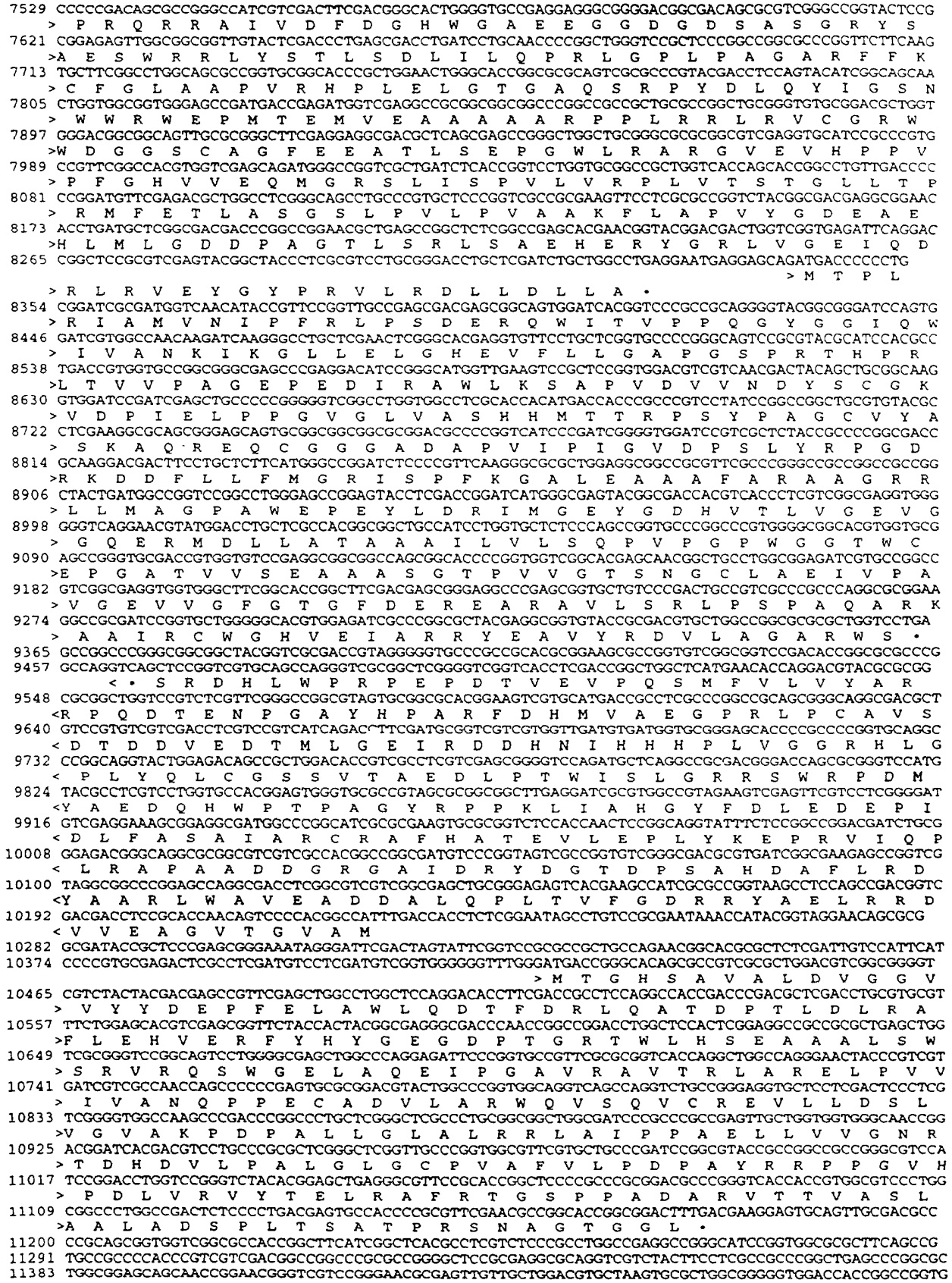


Figure 11B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>A E S W R R L Y S T L S D L I L Q P R L G P L P A G A R F F K
7713 TGCTTCGGCCTGGCAGCGCCGGTGCGGCACCCGCTGGAACTGGGCACCGGCGCGCAGTCGCGCCCGTACGACCTCCAGTACATCGGCAGCAA
> C F G L A A P V R H P L E L G T G A Q S R P Y D L Q Y I G S N
7805 CTGGTGGCGGTGGGAGCCGATGACCGAGATGGTCGAGGCCGCGGCGGCGGCCCGGCCGCCGCTGCGCCGGCTGCGGGTGTGCGGACGCTGGT
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7897 GGGACGGCGGCAGTTGCGCGGGCTTCGAGGAGGCGACGCTCAGCGAGCCGGGCTGGCTGCGGGCGCGCGGCGTCGAGGTGCATCCGCCCGTG
>W D G G S C A G F E E A T L S E P G W L R A R G V E V H P P V
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> R M F E T L A S G S L P V L P V A A K F L A P V Y G D E A E
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>H L M L G D D P A G T L S R L S A E H E R Y G R L V G E I Q D
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> M T P L
> R L R V E Y G Y P R V L R D L L D L L A •
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> I V A N K I K G L L E L G H E V F L L G A P G S P R T H P R
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> S K A Q R E Q C G G G A D A P V I P I G V D P S L Y R P G D
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> A A I R C W G H V E I A R R Y E A V Y R D V L A G A R W S •
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9457 GCCAGGTCAGCTCCGGTCGTGCAGCCAGGGTCGCGGCTCGGGGTCGGTCACCTCGACCGGCTGGCTCATGAACACCAGGACGTACGCGCGG
< • S R D H L W P R P E P D T V E V P Q S M F V L V Y A R
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10374 CCCCGTGCGAGACTCGCCTCGATGTCCTCGATGTCGGTGGGGGGTTTGGGATGACCGGGCACAGCGCCGTCGCGCTGGACGTCGGCGGGGT
> M T G H S A V A L D V G G V
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10925 ACGGATCACGACGTCCTGCCCGCGCTCGGGCTCGGTTGCCCGGTGGCGTTCGTGCTGCCCGATCCGGCGTACCGCCGGCCGCCGGGCGTCCA
> T D H D V L P A L G L G C P V A F V L P D P A Y R R P P G V H
11017 TCCGGACCTGGTCCGGGTCTACACGGAGCTGAGGGCGTTCCGCACCGGCTCCCCGCCCGCGGACGCCCGGGTCACCACCGTGGCGTCCCTGG
> P D L V R V Y T E L R A F R T G S P P A D A R V T T V A S L
11109 CGGCCCTGGCCGACTCTCCCCTGACGAGTGCCACCCCGCGTTCGAACGCCGGCACCGGCGGACTTTGACGAAGGAGTGCAGTTGCGACGCC
>A A L A D S P L T S A T P R S N A G T G G L •
11200 CCGCAGCGGTGGTCGGCGCCACCGGCTTCATCGGCTCACGCCTCGCCTGGCCGAGGCCGGGCATCCGGTGGCGCGCTTCAGCCG
11291 TGCCGCCCCACCCGTCGTCGACGGCCGGCCCGCGCCGGGGCTCCGCGAGGCGCAGGTCGTCTACTTCCTCGCCGCCCGGCTGAGCCCGGCGC
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Figure 11C

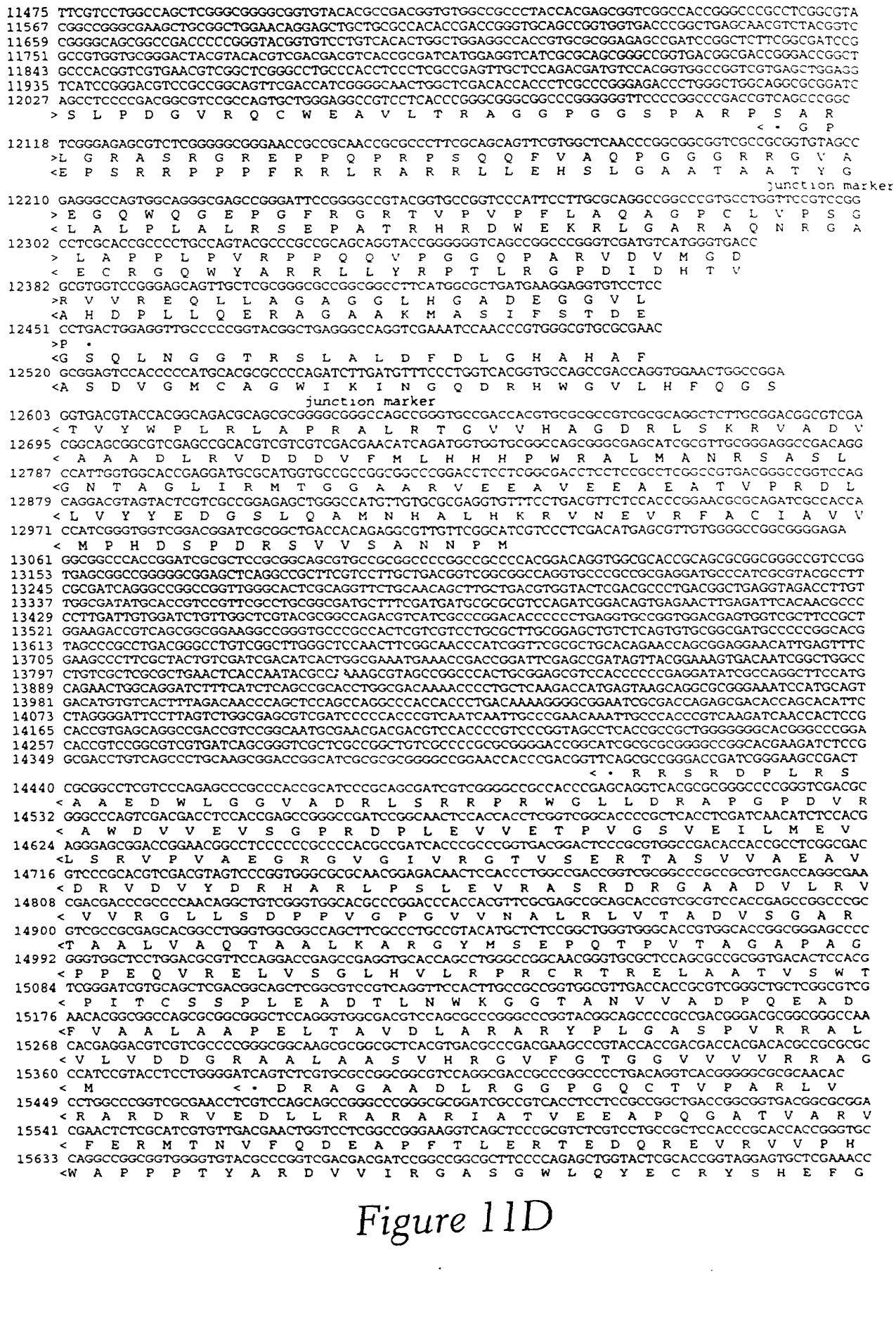
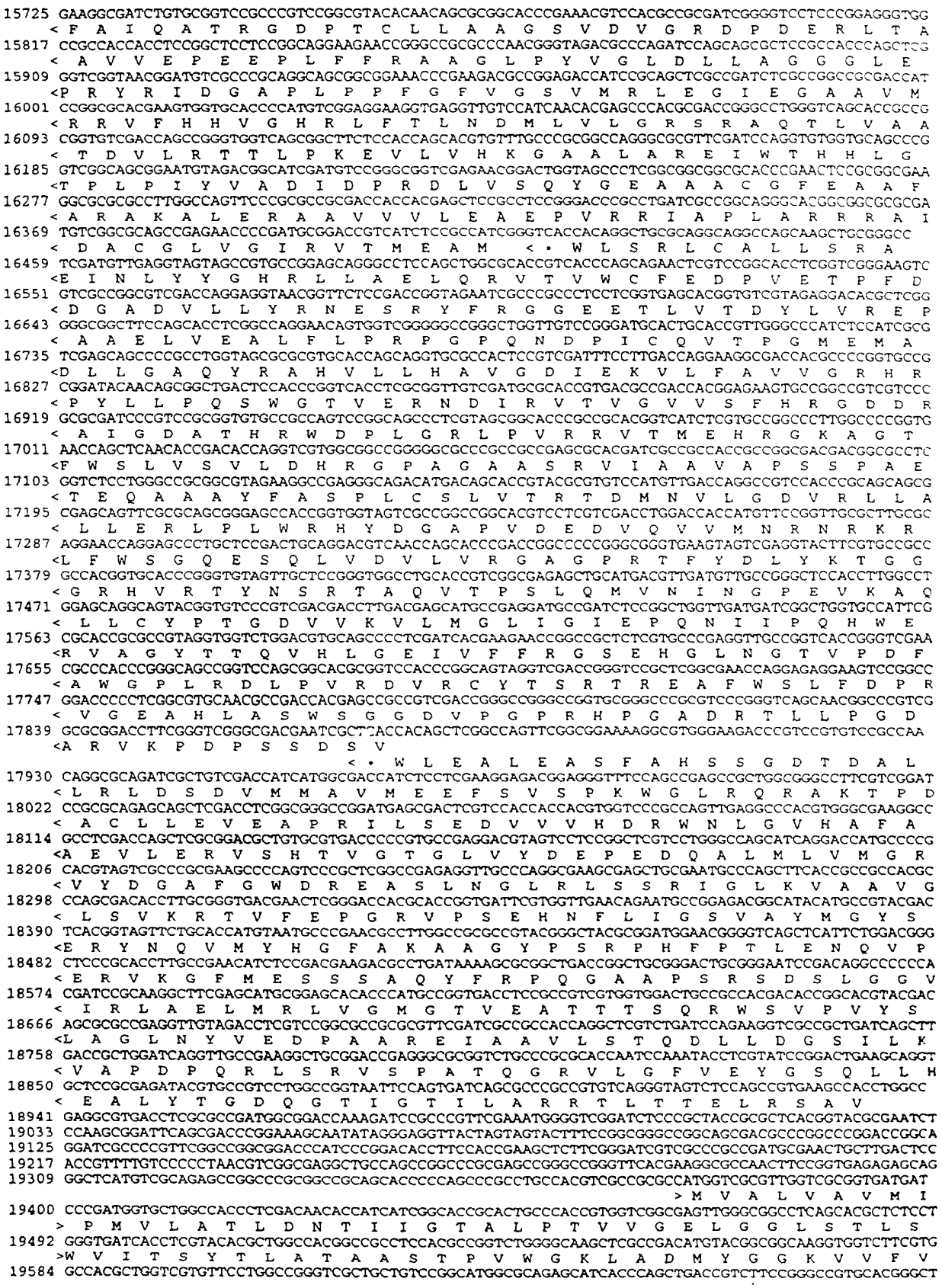


Figure 11D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< F A I Q A T R G D P T C L L A A G S V D V G R D P D E R L T A
15817 CCGCCACCACCTCCGGCTCCTCCGGCAGGAAGAACCGGGCCGCGCCCAACGGGTAGACGCCCAGATCCAGCAGCGCTCCGCCACCCAGCTCG
< A V V E P E E P L F F R A A G L P Y V G L D L L A G G G L E
15909 GGTCGGTAACGGATGTCGCCCGCAGGCAGCGGCGGAAACCCGAAGACGCCGGAGACCATCCGCAGCTCGCCGATCTCGCCGGCCGCGACCAT
<P R Y R I D G A P L P P F G F V G S V M R L E G I E G A A V M
16001 CCGGCGCACGAAGTGGTGCACCCCATGTCGGAGGAAGGTGAGGTTGTCCATCAACACGAGCCCACGCGACCGGGCCTGGGTCAGCACCGCCG
< R R V F H H V G H R L F T L N D M L V L G R S R A Q T L V A A
16093 CGGTGTCGACCAGCCGGGTGGTCAGCGGCTTCTCCACCAGCACGTGTTTGCCCGCGGCCAGGGCGCGTTCGATCCAGGTGTGGTGCAGCCCG
< T D V L R T T L P K E V L V H K G A A L A R E I W T H H L G
16185 GTCGGCAGCGGAATGTAGACGGCATCGATGTCCGGGCGGTCGAGAACGGACTGGTAGCCCTCGGCGGCGGCGCACCCGAACTCCGCGGCGAA
<T P L P I Y V A D I D P R D L V S Q Y G E A A A C G F E A A F
16277 GGCGCGCGCCTTGGCCAGTTCCCGCGCCGCGACCACCACGAGCTCCGCCTCCGGGACCCGCCTGATCGCCGGCAGGGCACGGCGGCGCGCGA
< A R A K A L E R A A V V V L E A E P V R R I A P L A R R A I
16369 TGTCGGCGCAGCCGAGAACCCCGATGCGGACCGTCATCTCCGCCATCGGGTCACCACAGGCTGCGCAGGCAGGCCAGCAAGCTGCGGGCC
< D A C G L V G I R V T M E A M < • W L S R L C A L L S R A
16459 TCGATGTTGAGGTAGTAGCCGTGCCGGAGCAGGGCCTCCAGCTGGCGCACCGTCACCCAGCAGAACTCGTCCGGCACCTCGGTCGGGAAGTC
<E I N L Y Y G H R L L A E L Q R V T V W C F E D P V E T P F D
16551 GTCGCCGGCGTCGACCAGGAGGTAACGGTTCTCCGACCGGTAGAATCGCCCGCCCTCCTCGGTGAGCACGGTGTCGTAGAGGACACGCTCGG
< D G A D V L L Y R N E S R Y F R G G E E T L V T D Y L V R E P
16643 GGGCGGCTTCCAGCACCTCGGCCAGGAACAGTGGTCGGGGGCCGGGCTGGTTGTCCGGGATGCACTGCACCGTTGGGCCCATCTCCATCGCG
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< P Y L L P Q S W G T V E R N D I R V T V G V V S F H R G D D R
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<F W S L V S V L D H R G P A G A A S R V I A A V A P S S P A E
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17471 GGAGCAGGCAGTACGGTGTCCCGTCGACGACCTTGACGAGCATGCCGAGGATGCCGATCTCCGGCTGGTTGATGATCGGCTGGTGCCATTCG
< L L C Y P T G D V V K V L M G L I G I E P Q N I I P Q H W E
17563 CGCACCGCGCCGTAGGTGGTCTGGACGTGCAGCCCCTCGATCACGAAGAACCGGCCGCTCTCGTGCCCGAGGTTGCCGGTCACCGGGTCGAA
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17747 GGACCCCCTCGGCGTGCAACGCCGACCACGAGCCGCCGTCGACCGGGCCGGGCCGGTGCGGGCCCGCGTCCCGGGTCAGCAACGGCCCGTCG
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< • W L E A L E A S F A H S S G D T D A L
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< A C L L E V E A P R I L S E D V V V H D R W N L G V H A F A
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< V Y D G A F G W D R E A S L N G L R L S S R I G L K V A A V G
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< L S V K R T V F E P G R V P S E H N F L I G S V A Y M G Y S
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< E R V K G F M E S S S A Q Y F R P Q G A A P S R S D S L G G V
18574 CGATCCGCAAGGCTTCGAGCATGCGGAGCACACCCATGCCGGTGACCTCCGCCGTCGTGGTGGACTGCCGCCACGACACCGGCACGTACGAC
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19033 CCAAGCGGATTCAGCGACCCGGAAAGCAATATAGGGAGGTTACTAGTAGTACTTTCCGGCGGGCCGGCCAGCGACGCCCGGCCCGGACCGGCA
19125 GGATCGCCCCGTTCGGCCGGCGGACCCATCCCGGACACCTTCCACCGAAGCTCTTCGGGATCGTCGCCCGCCGATGCGAACTGCTTGACTCC
19217 ACCGTTTTGTCCCCCTAACGTCGGCGAGGCTGCCAGCCGGCCCGCGAGCCGGGCCGGGTTCACGAAGGCGCCAACTTCCGGTGAGAGAGCAG
19309 GGCTCATGTCGCAGAGCCGGCCCGCGGCCGCAGCACCCCCAGCCCGCCTGCCACGTCGCCGCGCCATGGTCGCGTTGGTCGCGGTGATGAT
> M V A L V A V M I
19400 CCCGATGGTGCTGGCCACCCTCGACAACACCATCATCGGCACCGCACTGCCCACCGTGGTCGGCGAGTTGGGCGGCCTCAGCACGCTCTCCT
> P M V L A T L D N T I I G T A L P T V V G E L G G L S T L S
19492 GGGTGATCACCTCGTACACGCTGGCCACGGCCGCCTCCACGCCGGTCTGGGGCAAGCTCGCCGACATGTACGGCGGCAAGGTGGTCTTCGTG
>W V I T S Y T L A T A A S T P V W G K L A D M Y G G K V V F V
19584 GCCACGCTGGTCGTGTTCCTGGCCGGGTCGCTGCTGTCCGGCATGGCGCAGAGCATCACCCAGCTGACCGTCTTCCGGGCCGTGCACGGGCT

Figure 11E

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19676 CGGCGGCGGGCGGCCTGATGGTCTGCGCGTTCGCCATCATGGTGGAGGTTCTCGCCGGCCCTGACCTGCCCAAGTACCAGGGCATCATGTCGG
    > G A G G L M V C A F A I M V E V L A G P D L P K Y Q G I M S
19768 CGACCATGGGCCTGACCATGGTGGCGGGCCCGCTCGTCGGCGGCCTGATCACCGATGAGCTCGGCTGGCGCTGGTGCTTCTACATCAACCTG
    >A T M G L T M V A G P L V G G L I T D E L G W R W C F Y I N L
19860 CCGATCGGGGCGGTCGCGCTGCTCATCGTGGTGCTGATGATGCACCTGCCGCGCCGACACACCAAGGCCCGGATCGATTACGCGGGTGCTGC
    > P I G A V A L L I V V L M M H L P R R H T K A R I D Y A G A A
19952 CCTGCTCACCGTGGTCAGTTCGTGCGTCGTGCTGGTGACCACCTGGGGCGGCATCACCTACCCCTGGGCGTCTCCGATGATCCTGGGGCTGG
    > L L T V V S S C V V L V T T W G G I T Y P W A S P M I L G L
20044 TCGCGCTCGGGGTGCTGACCTGCGCGCTCTTCGTGGTGGTCGAGCGACGGGTGGCCGAGCCGTTGGTGCCCCTGGCCATGTTCCGCAGCCTG
    >V A L G V L T C A L F V V V E R R V A E P L V P L A M F R S L
20136 AACTTCACCCTGAGCACCCTCATCGCCTTCCTGGTCGGCTTCGCCCTCATCGCGGGGCTGACCTTCCTGGCCCTGTTCCAGCAGGCGGTGCA
    > N F T L S T L I A F L V G F A L I A G L T F L A L F Q Q A V Q
20228 GGGTGCCTCCGCGTCCGACTCCGGCCTGTTGCTGCTGCCCCTGCTGCTGTCCATGGCGGCGGTCAACGTGGTCGGGGGTCGCCTGATGAGCG
    > G A S A S D S G L L L L P L L L S M A A V N V V G G R L M S
20320 GCGGGCGTTCCTACCGGCTGCTGATGCTCGCCGGTGCGGCGCTGATGACCCTGAGCCTGCTGCTCTTCGCCCTGATGGACGTGGGCACCAGC
    >G G R S Y R L L M L A G A A L M T L S L L L F A L M D V G T S
20412 CGGACGGTCACCGCGATCCCCATGGTCGGCTTCGGCGCAGGGCTGGGGCTGCTCATGCAGACCAGCCTGATGGTGGCGCTGAGCAGCGTGGA
    > R T V T A I P M V G F G A G L G L L M Q T S L M V A L S S V E
20504 GATGAGGAACCTCGGGGTGGCCGCCTCCACGTCCACGCTCTTCCGCACCATCGGTGGGGCGGTGGGGGCGTCGGCGACGGTCTCGCTGTTCT
    > M R N L G V A A S T S T L F R T I G G A V G A S A T V S L F
20596 CCGTGCGGGTGCAGTCGGCGCTGGCCGATCGGGGGGTCGCCGACGTGGCTGACCTCCTCGGCCACTCCGCGCGGCTGGACGCCGCCGGGCTG
    >S V R V Q S A L A D R G V A D V A D L L G H S A R L D A A G L
20688 GCCCAACTCCCCCGGGCCGTCCGTGTCCACTTCATGCACGCGGTGGCCTCCGGCACCCGGTGGGCCTTCCTGATGACCGTGCTGGCGGGGCT
    > A Q L P R A V R V H F M H A V A S G T R W A F L M T V L A G L
20780 GATCTGCGTCGCGGCGGCGTGGTTCCTGCGCCGGGTCACCCCGTTGACGTCGGCACCGGTGGCACCCGAACCGGCGCGCGACGTCGCCGCGC
    > I C V A A A W F L R R V T P L T S A P V A P E P A R D V A A
20872 CCGCCGCCAGCAGCGGGCGCGCCGAACTACTAGCGGATTTCCTAGGGTTCCTCGTCGACGGTAGAGCTGAATTCACCGGCGACCTAACA
    >P A A S S G R A P N Y •
20963 TTCTTTTCGCGATCCGGAATCCGTCCATTCCCCTGTCTGGCGATGGTCGACGGGCCGGCCCGTGCCGAGCGGACAGACACAGATTCTCGGAT
21055 TGGAGCTCGATGTCCAGCAAGATCCTAGTCATCGGTGGAGGTCCGGCCGGATCCACGGCCGCCGCGCTGCTCGCCCGATCGGGGCTGTCG
                >M S S K I L V I G G G P A G S T A A A L L A R S G L S
21145 GTGACGCTCCTGGAAAAGGAGACGTTCCCGCGATACCACATCGGCGAGTCGATCGCGTCCTCGTGCCGCACCATCGTCGATTTCGTGGGCGC
    > V T L L E K E T F P R Y H I G E S I A S S C R T I V D F V G A
21237 TCTCGACGAGGTCGACTCGCGGGGCTACCCGCAGAAGAACGGGGTCCTGCTGCGCTGGGGCAACGAGGACTGGGCCATCGACTGGGCCAAGA
    > L D E V D S R G Y P Q K N G V L L R W G N E D W A I D W A K
21329 TCTTCGGTCCGGGCGTGCGGTCCTGGCAGGTCGACCGGGACGACTTCGACCACGTCCTGCTCAACAACGCCGGCAAGCAGGGCGCCAAGATC
    >I F G P G V R S W Q V D R D D F D H V L L N N A G K Q G A K I
21421 ATCCAGGGCGCGGCTGTCAAGCGGGTGTTGTTCGACGGTGAGCGGGCCACCGCCGCCGAGTGGTTCGACCCCGAGTCGGGTGAGGTCCGCAC
    > I Q G A A V K R V L F D G E R A T A A E W F D P E S G E V R T
21513 CATCGATTTCGACTACGTGGTCGACGCGTCCGGCCGGGCCGGGCTGATCCCGTCCCAGCACTTCAAGCACCGGCGCCCCACCGAGACGTTCA
    > I D F D Y V V D A S G R A G L I P S Q H F K H R R P T E T F
21605 AGAACGTGGCCATCTGGGGCTACTGGCAGGGTGGCTCGCTGCTGCCGAACTCTCCCTCCGGCGGGATCAACGTCATCTCCGCGCCCGACGGC
    >K N V A I W G Y W Q G G S L L P N S P S G G I N V I S A P D G
21697 TGGTACTGGGTCATTCCGCTGCGCGGCGACCGGTACAGCATCGGCTTCGTCTGCCACCAGAGCCGCTTCCTGGAGCGGCGCAAGGAGCACGC
    > W Y W V I P L R G D R Y S I G F V C H Q S R F L E R R K E H A
21789 CTCGCTGGAGGACATGCTCGCCGCACTGGTACAGGAGTCCCCGACCGTGCGCGGCCTGACGGCGAACGGGACGTACCAGCCGGGCGTGCGGG
    > S L E D M L A A L V Q E S P T V R G L T A N G T Y Q P G V R
21881 TGGAGCAGGACTTCTCGTACATCTCCGACAGCTTCTGCGGGCCCGGCTACTTCGCGGCCGGCGACTCCGCCTGCTTCCTGGACCCACTGCTG
    >V E Q D F S Y I S D S F C G P G Y F A A G D S A C F L D P L L
21973 TCCACCGGCGTGCACCTCGCCCTCTACAGCGGCATGCTCGCCTCGGCGTCCATCCTGGCCACCATCCACGGTGACGTCACCGAGGAGGAGGC
    > S T G V H L A L Y S G M L A S A S I L A T I H G D V T E E E A
22065 GCGGGCGTTCTACGAGTCCCTCTACCGCAACGCCTACCAGCGCCTGTTCACCCTCGTCGCCGGCGTCTACCAGCAGCAGGCCGGCAAGAGGG
    > R A F Y E S L Y R N A Y Q R L F T L V A G V Y Q Q Q A G K R
22157 CATACTTCGGCCTGGCCGACGCGCTGGTGCACGACAGCGGCGAACCCGAGTACGAGAAGGTAGACGGGGCCCGCGCCTTCGCCCAGCTCGTC
    >A Y F G L A D A L V H D S G E P E Y E K V D G A R A F A Q L V
22249 GCCGGCCTCGCCGACCTGGACGACGCGGCGGAGGGACGGCACGACAGCACCGCGGCGGCGGCACCGGCGGAGCAGGACAACTCCGTCCGGCA
    > A G L A D L D D A A E G R H D S T A A A A P A E Q D N S V R Q
22341 GCTCTTCCTGGCCGCCGAGGAGGCCCGCCGGATGGCCGACGCGCGCACGCCGAGCGCCCCGGTCAGCGAGGCGCCGGGCAAGCTCGACAGCC
    > L F L A A E E A R R M A D A R T P S A P V S E A P G K L D S
22433 ACGACCTCTTCGACTCGGCAACCGGCCTCTACCTGGTCACCACCCCGCGACTGGGGATCCGCCGGGCCAAGCCGGCCGACACGCAGGCGGCG
    >H D L F D S A T G L Y L V T T P R L G I R R A K P A D T Q A A
22525 GCAGAGCAGTCTGCCTGAGGTTCCACCCCTGGTGGCCCCCGGCCCGGACCGCGCCGGTCCGGGGGCTGCTCAACCCTCCCACCAACATCCG
    > A E Q S A •
22616 GCATCCGGTGCCGGCGGCTGAGCAGGGGCAGCGCCACCGACTCCGGCCCGTCACATGGACAAGGTCACCTCTCCCGTGCTGAACAGACGACA
22708 GTTGCTCGCCCTCGGCAGCGTGGCCGCCGGAGGCACCGTCATGTCACGCTCCCTCAGACGGGACGCGCAGGCCGCCCAGGCGGCACCGGC
                                                    >M S R S L R R D A Q A A Q A A P A
22798 GTCGCCCGCCAACCCGCACGCCGGGCACGCCGCCCCGGTGCCCAGCCGGGTCAGCACGACCACGGTCGCGGTCACCCCGTTCACCGAGCCGA
    > S P A N P H A G H A A P V P S R V S T T T V A V T P F T E P
22890 TGCCCGTCCCGCCGCGGCTGACCCCGGTCTCCCGCCGCGACGGCATCGACGTCTACGAGATCCCCATCCGGCCGGCGCAGGTGCAGATCCTG
    >M P V P P R L T P V S R R D G I D V Y E I P I R P A Q V Q I L
22982 CCCGGCCTGCTCACGCCCGCCTACACCTACGCCGGTTCCTTCGTCGGCCCCACCATCCGGGCCCGCACGGGCCGGCCCGTGCGGATCACCTA
    > P G L L T P A Y T Y A G S F V G P T I R A R T G R P V R I T Y
23074 CACCAACGGGCTCGACACCCACGCCAACGTGCACCTGCACGGCGGGCACGTGCCGGCCACCAGCGACGGTCACCCGATGGACCTGATCCCGC
    > T N G L D T H A N V H L H G G H V P A T S D G H P M D L I P
23166 CGGGCGGCTCGAAGGTCTACGACTACCCGAACCTTCAGCGCGGCGCGACGCTCTGGTACCACGACCACACCCACGCCTACGAGGCCGACCAC
    >P G G S K V Y D Y P N L Q R G A T L W Y H D H T H A Y E A D H
23258 GTCTACCGCGGACTGCACGGCTTCTATCTGATCGACGACCCGGCCGAGCATCACCTGCGCCTGCCCGCCGGCAAGTACGACGTGCCGATCAT
    > V Y R G L H G F Y L I D D P A E H H L R L P A G K Y D V P I M
23350 GCTGCGCAACGCCCAGTTCGACGACTCCGGCGCCCTCGTCTTCGGCCACCCGGACGACCGGGTCACCATCCTGGCGAACGGCAAGGCCCAGC
    > L R N A Q F D D S G A L V F G H P D D R V T I L A N G K A Q
23442 CCTACTTCGAGGTGGCCCCGCGCAGGTACCGGTTCCGCCTGCTCAACGCGGCGCTGAAGCACGTCTTCCGGCTCAACCTGGGCGGCGAACCG
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Figure 11F

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    >P Y F E V A P R R Y R F R L L N A A L K H V F R L N L G G E P
23534 CTCACCCGCATCGCCACGGACGGCGGGCTGCTGCCCGCCCCCACCAGTCACACCGAGCTGGCGCTCTCCTCCGGGGAGCGGGTCGAGATTGT
    > L T R I A T D G G L L P A P T S H T E L A L S S G E R V E I V
23626 GATCGACTTCGCCGAGCACGCAGGCGGCGGGCCGGTCTACCTCTACGACGGGGACAACCCGATCCTGCGCTTCGACGTGTCGTCCCGGGCGG
    > I D F A E H A G G G P V Y L Y D G D N P I L R F D V S S R A
23718 TCACCGACCCCAGCCGGGTGCCGGTCACCCTGCGCGCACTGCCCCCGATGGGCACGCCGACCGTGGAGCGCACCGTGTCGATGAGCTTCGAC
    >V T D P S R V P V T L R A L P P M G T P T V E R T V S M S F D
23810 ATGTCGGCCCGGCCCCCGATCGCGCTCATGGACGGCAAACCGTTCGACCCTCTCCGGGTGGACGTACAGGTCAAGCGGGGCAGCACCGAGAT
    > M S A R P P I A L M D G K P F D P L R V D V Q V K R G S T E I
23902 CTGGAACGTGGTCAACGCGGATACCGATCCGTTCCCCTTCGACCATCCGTTCCACCTGCACCTGGTGACGTTCCGGGTGCTCGGCCGCGACG
    > W N V V N A D T D P F P F D H P F H L H L V T F R V L G R D
23994 GCGGGCCGCCCGCGCCGGAGGACGCCGGGCTCAAGGACACCGTCTACGTCTCGCCCAAGGGGTCTGTCAAGATCCAGGTCACCTTCGCCACG
    >G G P P A P E D A G L K D T V Y V S P K G S V K I Q V T F A T
24086 CCGTACCTCGGGCAGTACGTCTACCACTGCCACTACCTGGAGCACTCGTCGCTGGGGATGATGGCCCAGCTGGAGGTTGTGCCCTGAGGGC
    > P Y L G Q Y V Y H C H Y L E H S S L G M M A Q L E V V P •
24177 TCAGCCGTGCAGGTCGACGATCGAGGGGTGGGCGCCGAACAGGCTGACCGGCCGCACGTCGCCCACCCCGAACCCGGCGGCGCGGGCCAGG
    < • G H L D V I S P H A G F L S V P R V D G V G F G A A R A L
24268 TCGGCCTGGTCGGCGAACTCGTGCAGCAGCAGTACCGCCCGCCCGCCGTCGACCGTCACCCGGCGCAGCTCCGCGAAGAGGCGGCCGGAATC
    <D A Q D A F E H L L L V A R G G D V T V R R L E A F L R G S D
24360 ACCGGCGAGCACGCCCCGCGCCTGCACCTGCCGGTCCCAGGGCGGATTGCTGACCACCCGGTCCACCCGACCGGTCCGCAGCGGCAATCGTC
    < G A L V G R A Q V Q R D W P P N S V V R D V R G T R L P L R G
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Figure 11G

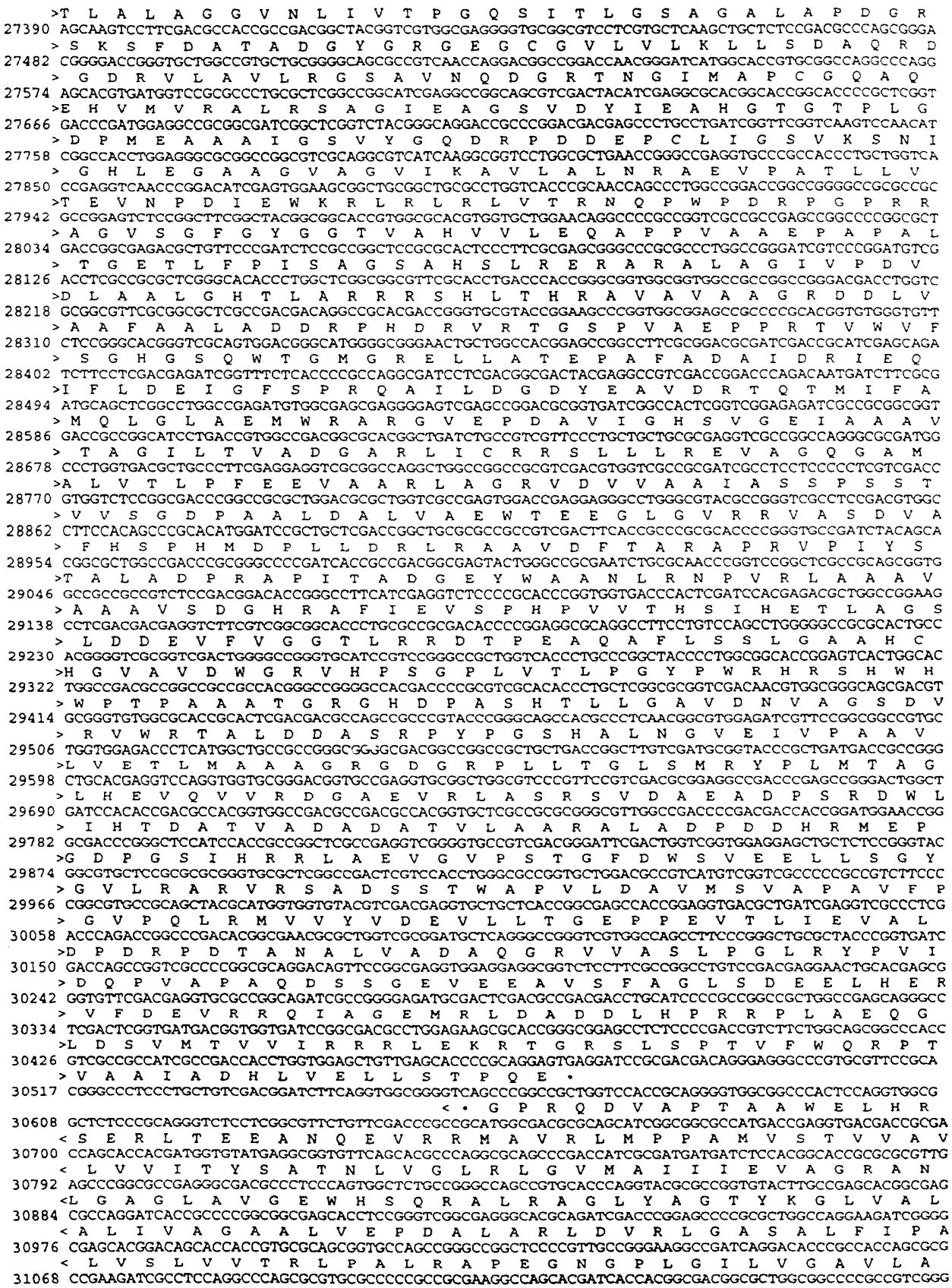
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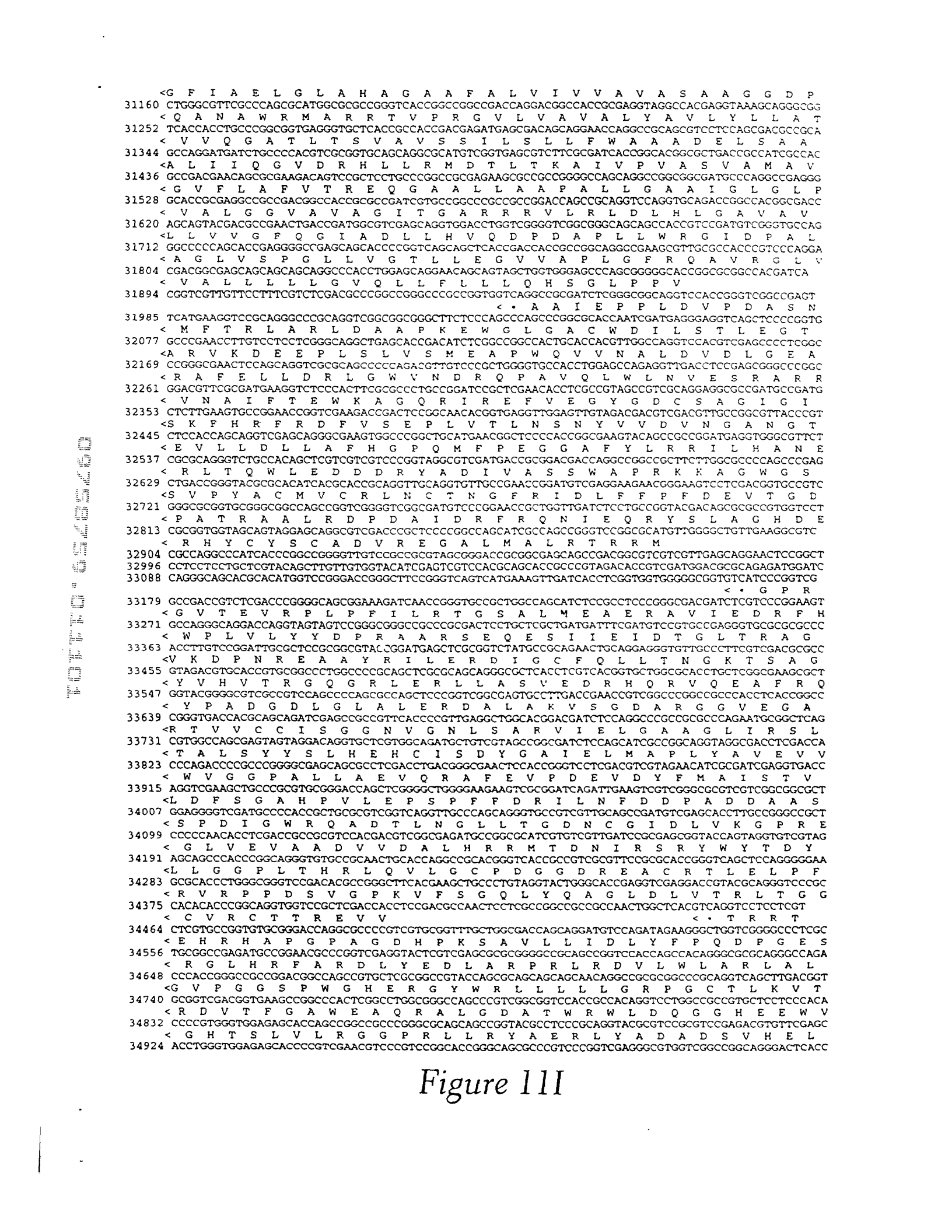
Figure 11H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< W V G G P A L L A E V Q R A F E V P D E V D Y F M A I S T V
33915 AGGTCGAAGCTGCCCGCGTGCGGGACCAGCTCGGGGCTGGGGAAGAAGTCGCGGATCAGATTGAAGTCGTCGGGCGCGTCGTCGGCGGCGCT
<L D F S G A H P V L E P S P F F D R I L N F D D P A D D A A S
34007 GGAGGGGTCGATGCCCCACCGCTGCGCGTCGGTCAGGTTGCCCAGCAGGGTGCCGTCGTTGCAGCCGATGTCGAGCACCTTGCCGGGCCGCT
< S P D I G W R Q A D T L N G L L T G D N C G I D L V K G P R E
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< G L V E V A A D V V D A L H R R M T D N I R S R Y W Y T D Y
34191 AGCAGCCCACCCGGCAGGGTGTGCCGCAACTGCACCAGGCCGCACGGGTCACCGCCGTCGCGTTCCGCGCACCGGGTCAGCTCCAGGGGGAA
<L L G G P L T H R L Q V L G C P D G G D R E A C R T L E L P F
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< R V R P P D S V G P K V F S G Q L Y Q A G L D L V T R L T G G
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< C V R C T T R E V V <• T R R T
34464 CTCGTGCCGGTGTGCGGGACCAGGCGCCCCGTCGTGCGGTTTGCTGGCGACCAGCAGGATGTCCAGATAGAAGGGCTGGTCGGGGCCCTCGC
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Figure 111

```
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35290 AGGGTCACCAACGCCAGTACTCCTCGTGCGGGTACCGCATGGTGGTCGGCTCCGGCAGGCCCTCCCAGCGCCGCAGCGACGCGGCGGGCCG
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35657 CCGGGTGGTGGTCTCGTTCGCCCGGTCGGTGTCCCAGTAGTTCGACTGCGGGATGCACCAGACGCAGTTGTCCTCCGGGGCCGGGTCAAGGT
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35841 GCCCCCGCCTCGGTCTTGAAGACCATGCTGTCCCAGGTGGGGATGAGGTTGGGGCCGACCAGGTCCTCCATCGCCCGCAGCAGCAGGGGGTG
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36576 TGACCAGGTCGATCCGGCGGTCACCGGGGAGCACGTCGTCCAGGCGGACGGTGTCGACCGTCAGCTCCCGCAGGGTCTCGTCCGGGCGGTCG
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    <Q  D  Y  W  D  N  M
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37403 GACGCCGGCCTCCTGGCAGCGGGGCAGCACCTCCTTCTCGGCACCACGGTCGAGCAGGTTGAACGGCACCTGGACGACGTCCAGCAGCCCGG
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38046 CCCCACCCACGCCCGTCGGCCGGCCGTCACGCCGCCGGCTCCCCGTCGCTGCGCAGCGTCAGGAACACCACGCCGTCGTGATTGATCATCT
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38413 CGGCGGTCGGCAGCTTCTCCAGGAAGTCGTTCTCGATGTGGTGGTAGGAGACGTTCTCCCGGCCCTCGCAGGTGGCGCGCGCCTTGTCGAGG
    <  A  T  P  L  K  E  L  F  D  N  E  I  H  H  Y  S  V  N  E  R  G  E  C  T  A  R  A  K  D  L
38505 AAGGATCGGCTGACGTCGGCGCAGAGCACGGCGCGCACCCGGTCGGCGAGCCCGGCCGCCATGATGCCCTCGCCGCTGCCGATCTCGAAGAT
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38597 CTCCGATTCCGGGCCGAGCCCGAGCTGCTCGACGACCAGGGCGACCTTGTCGACACGGTCCTGGAGGTACTCCTCGCGCGGCTGGTAGCCGG
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9,956,154 B2

Figure 11J

09/759,548

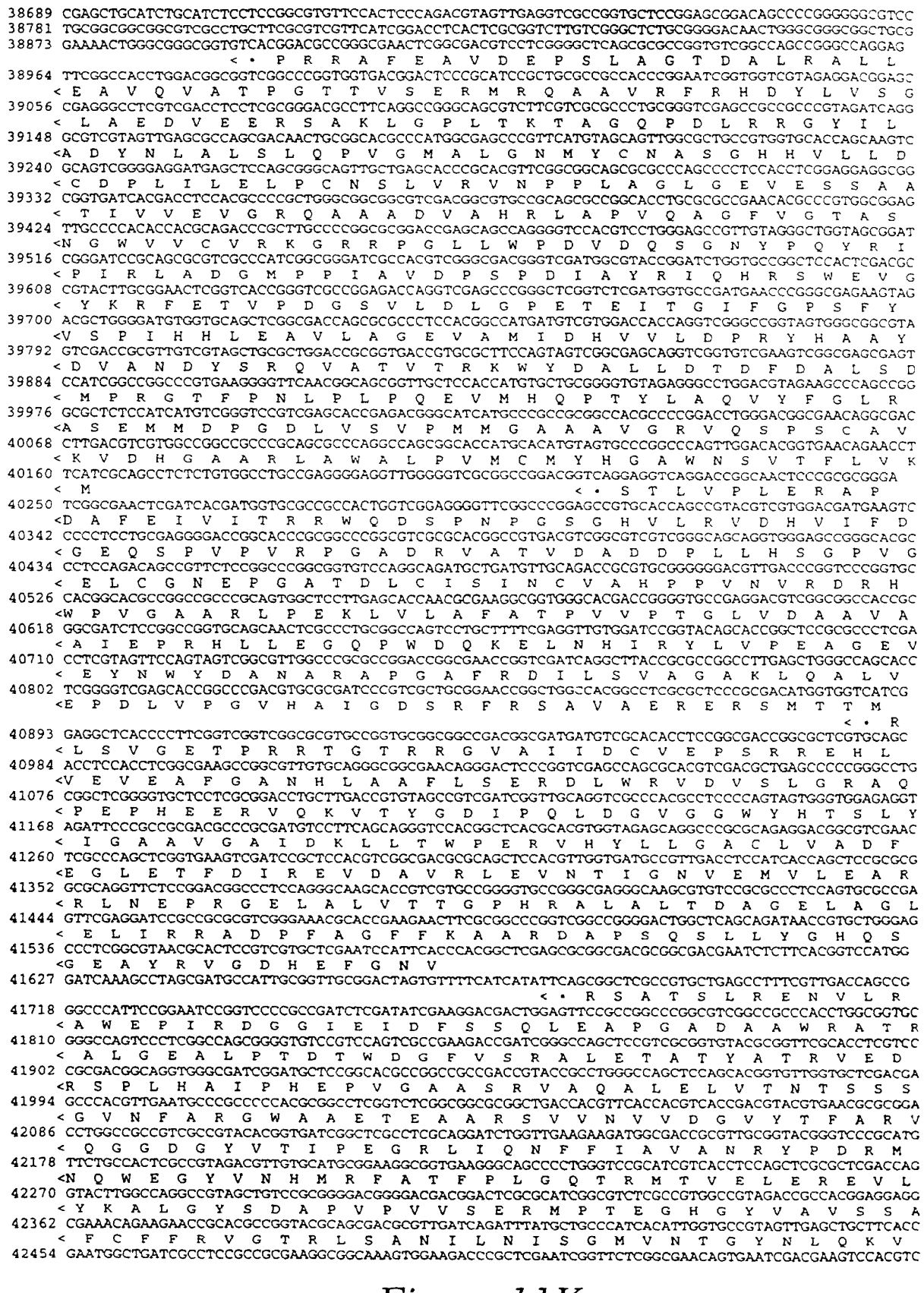

Figure 11K

```
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42546 GGTCACCGAACCGACGGCCAGGTCCACCCCGGCCGGAACCCGCTGCCGGCTGCCGCCGCTGAGGTCGTCCAGAACGGTGACCCGGTGCCCAT
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42819 CGGCGACCGGTCGGCCTGCTTCTTCAGCGGCTCCCACCAGTCCCGGTGCGTCCGGTACCAGTCGATCGTCTCGGCCAGGCCGTCGGCGAAGG
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42911 CGACCTCGGGCCGGTAGCCGAGCGCCCGCAGTTTCGCGTCCGTCAGCGAGTAGCGGCGGTCGTGGCCCTTGCGGTCCGGCACCCGCTCGACC
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95595 30 1 PCT/US95/14

Figure 11L

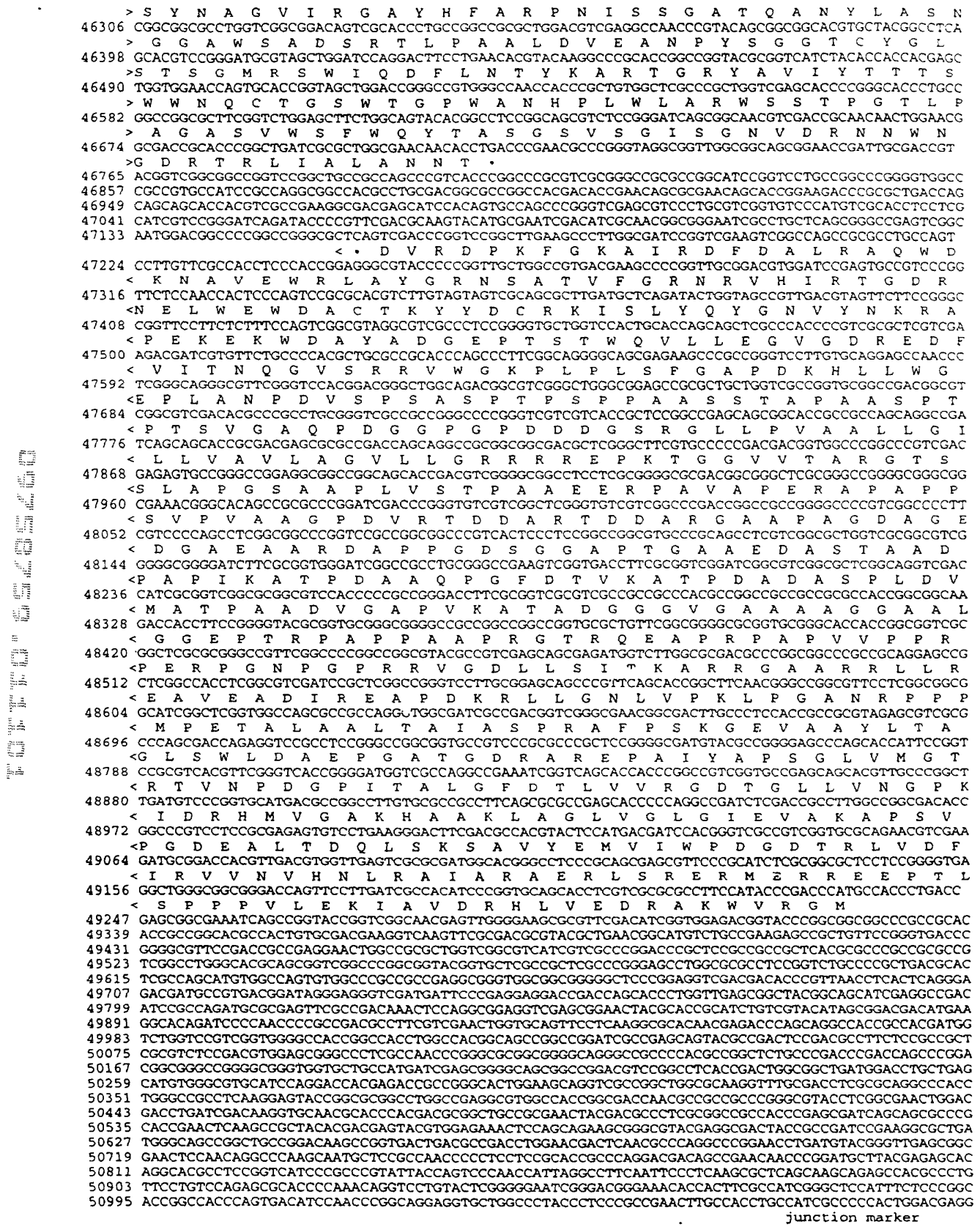

Figure 11M

Figure 11N

US 6,054,564 A

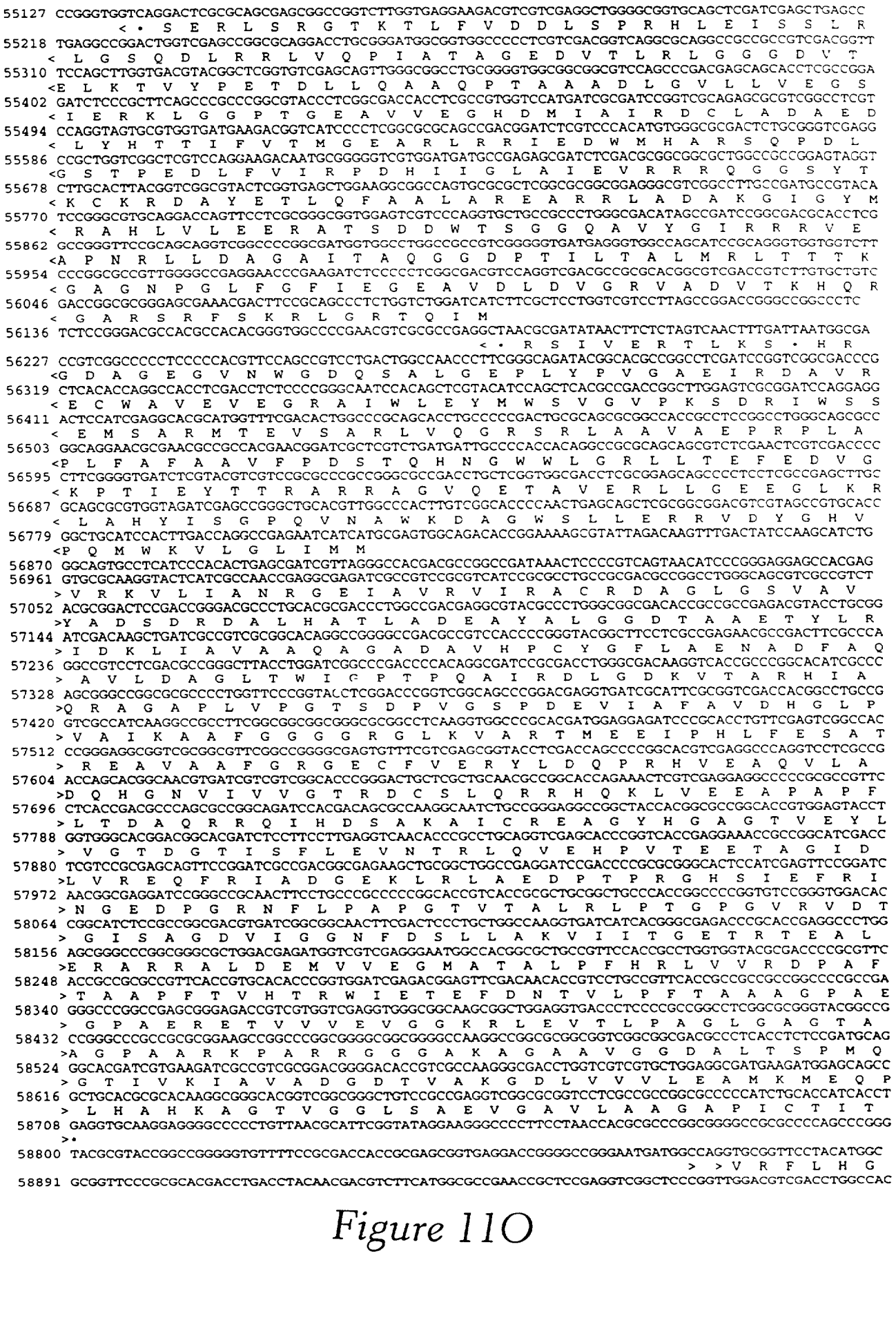

Figure 11O

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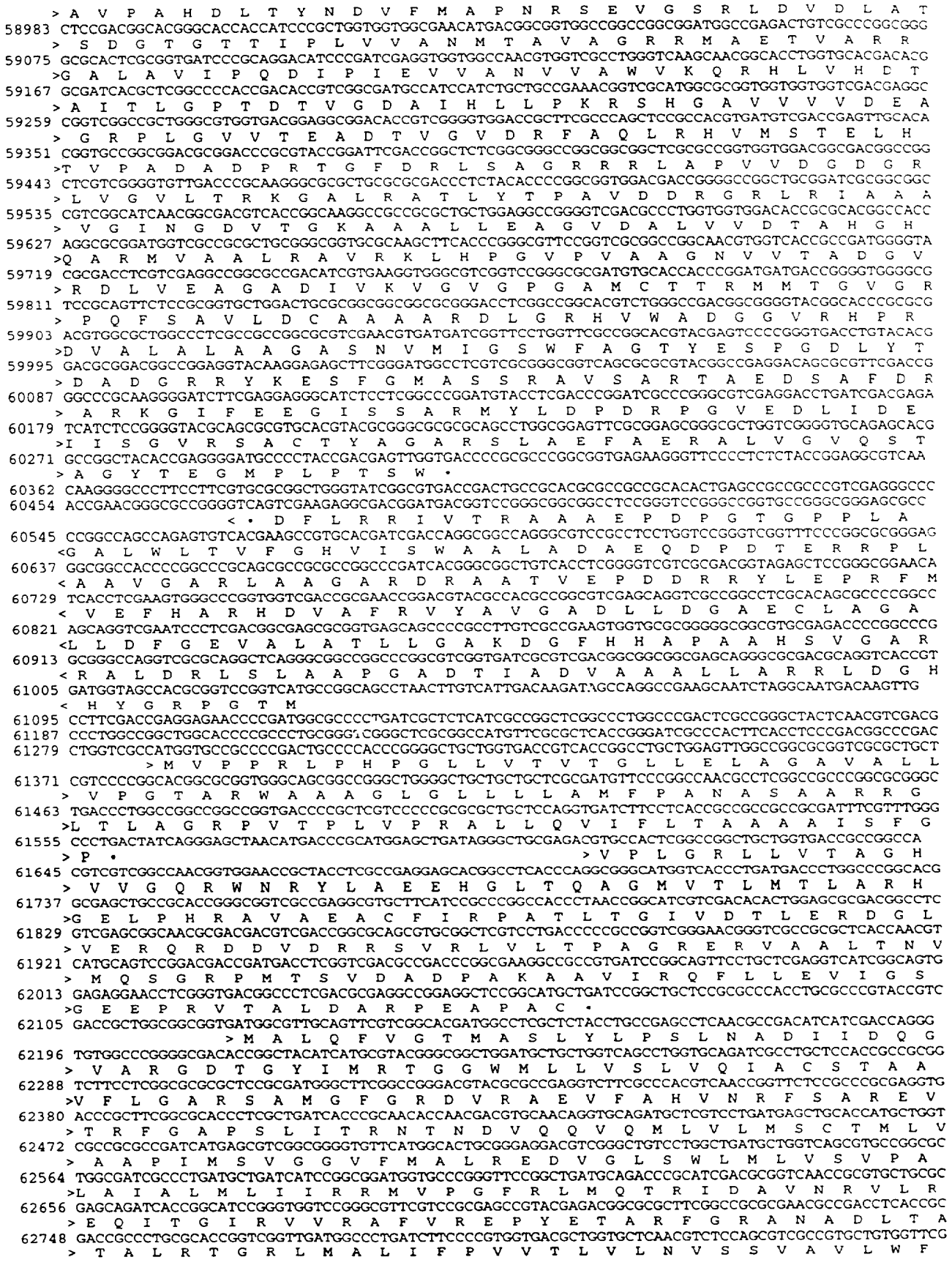

Figure 11P

PCT/US99/26559

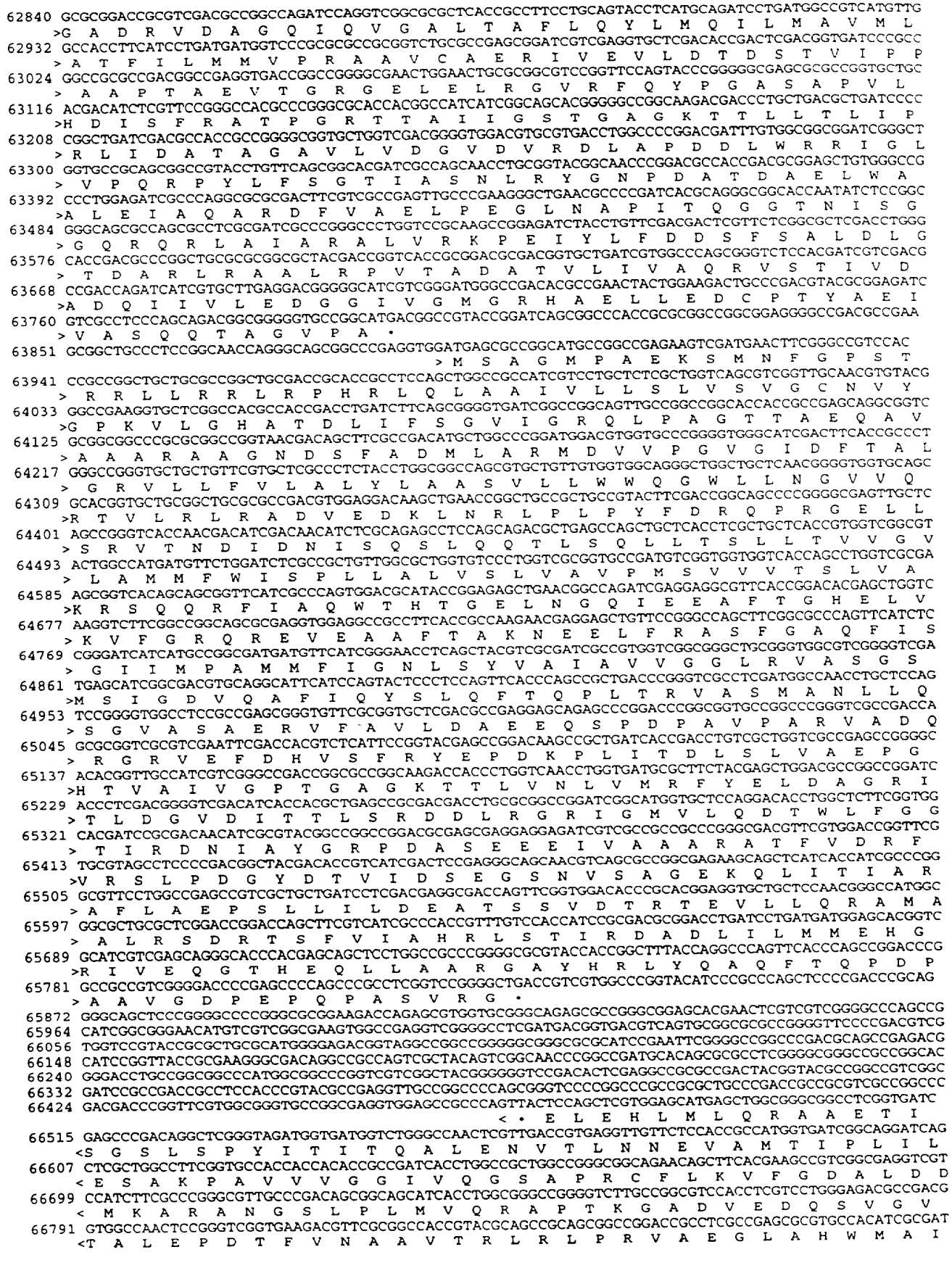

Figure 11Q

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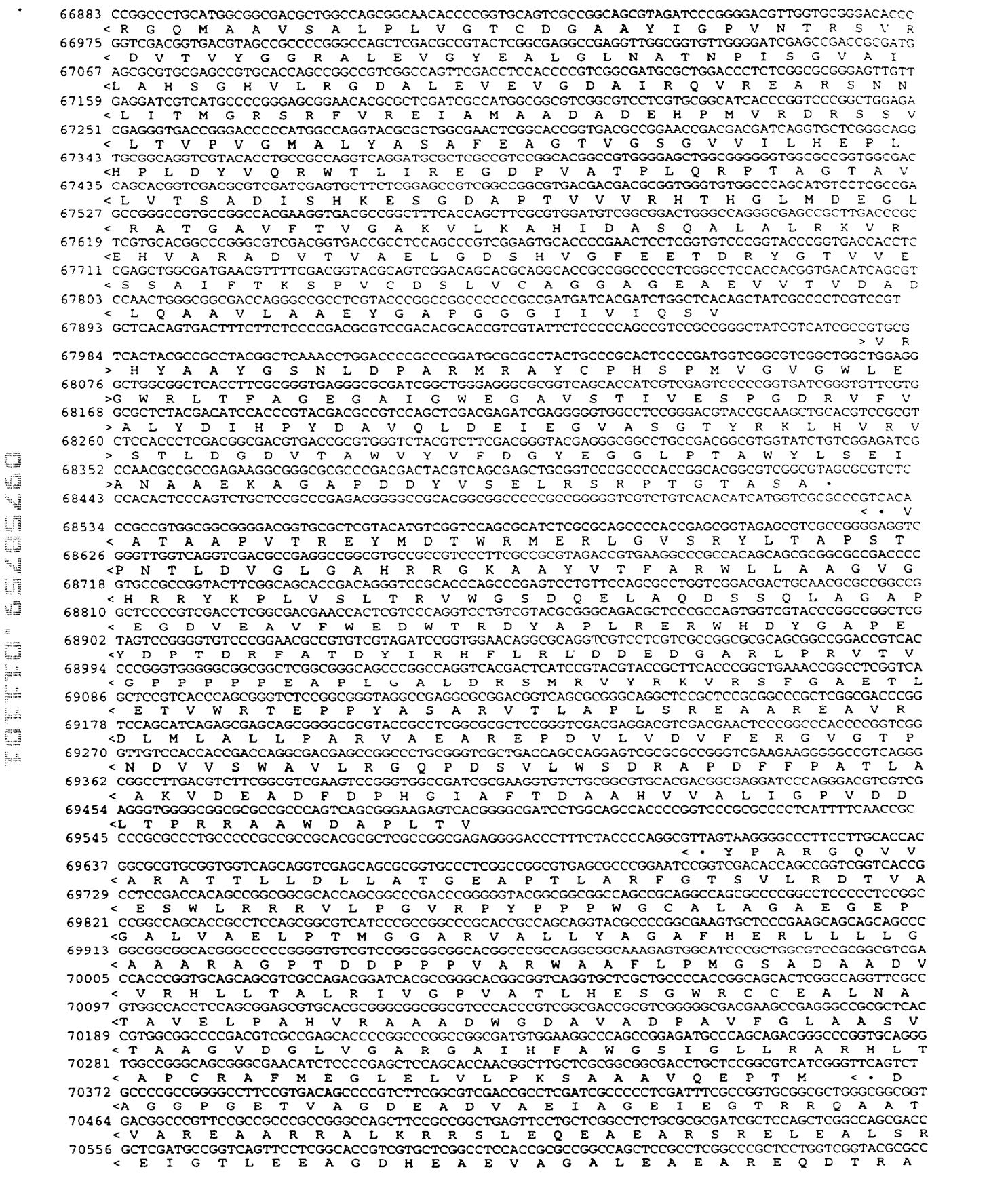

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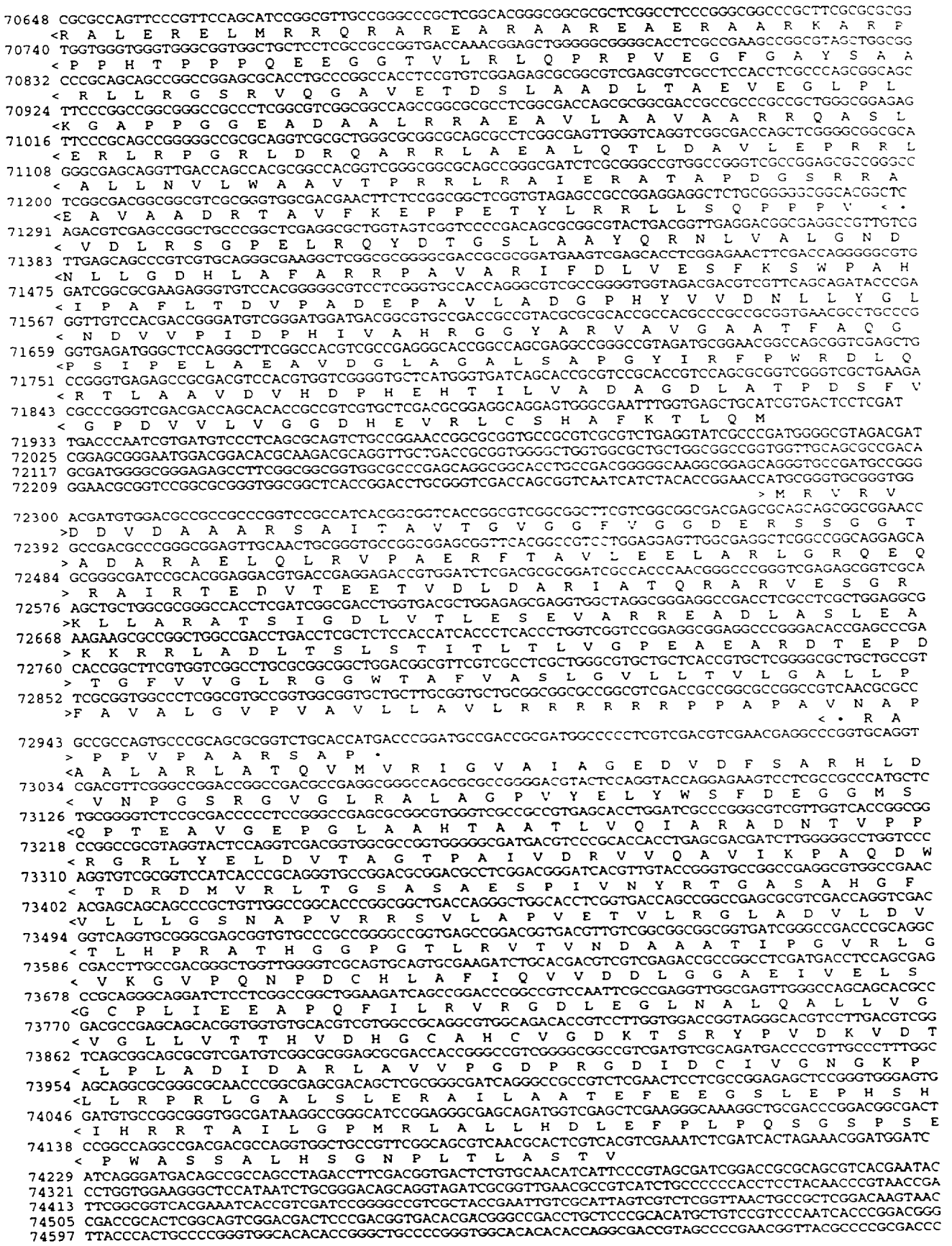

Figure 11S

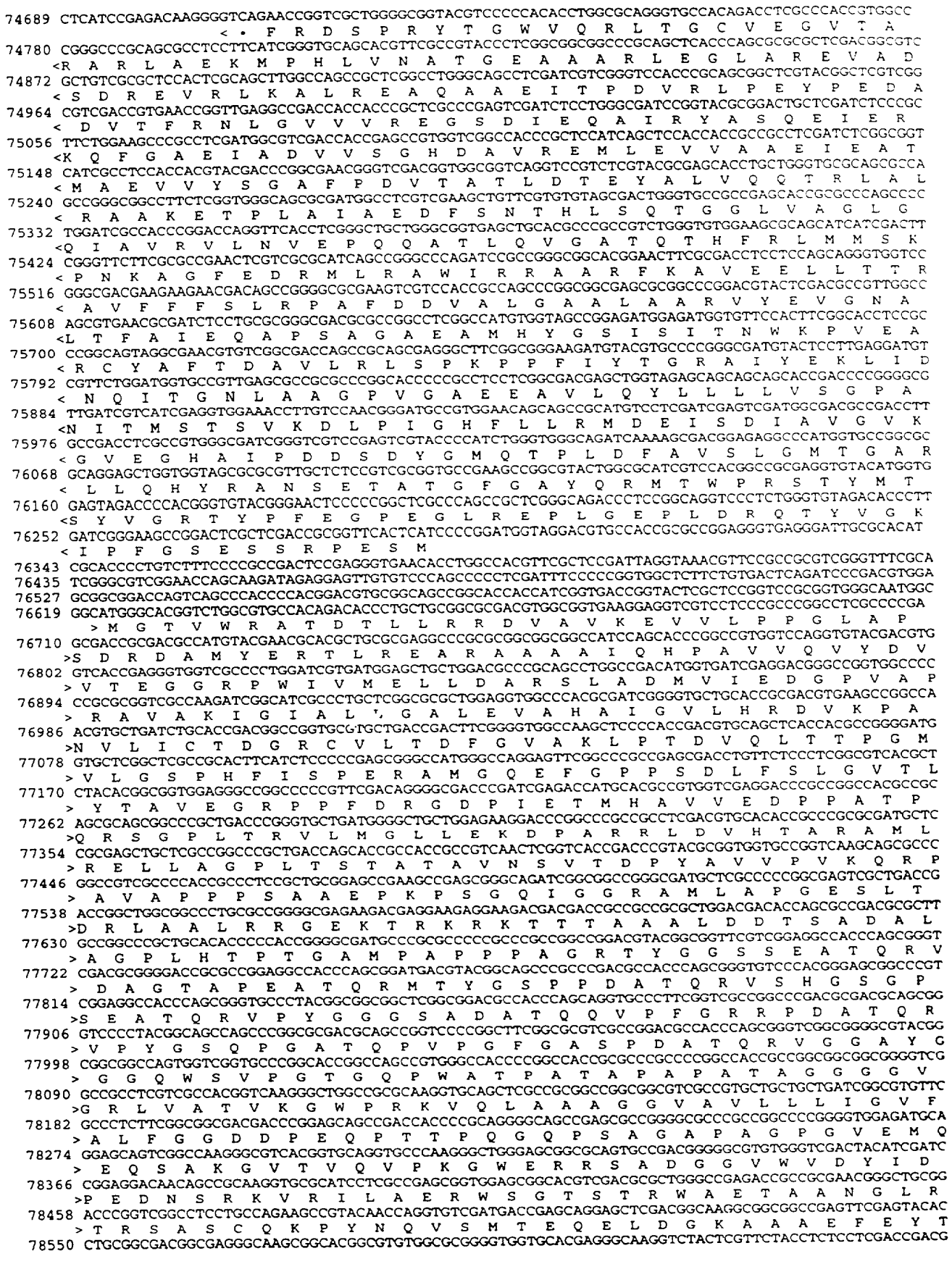
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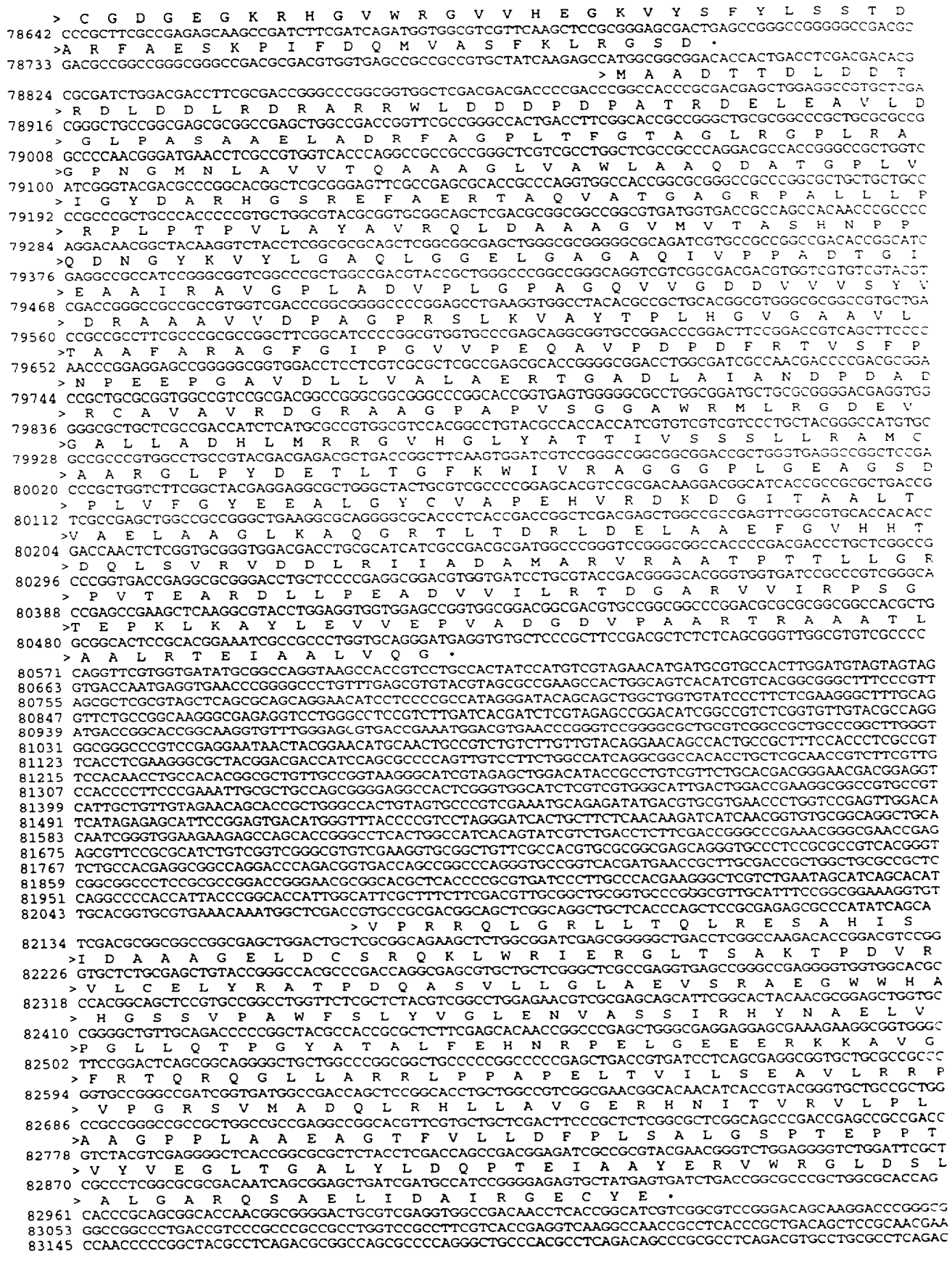
Figure 11T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81123 TCACCTCGAAGGGCGCTACGGACGACCATCCAGCGCCCCAGTTGTCCTTCTGGCCATCAGGCGGCCACACCTGCTCGCAACCGTCTTCGTTG
81215 TCCACAACCTGCCACACGGCGCTGTTGCCGGTAAGGGCATCGTAGAGCTGGACATACCGCCTGTCGTTCTGCACGACGGGAACGACGGAGGT
81307 CCACCCCTTCCCGAAATTGCGCTGCCAGCGGGGAGGCCACTCGGGTGGCATCTCGTCGTGGGCATTGACTGGACCGAAGGCGGCCGTGCCGT
81399 CATTGCTGTTGTAGAACAGCACCGCTGGGCCACTGTAGTGCCCGTCGAAATGCAGAGATATGACGTGCGTGAACCCTGGTCCGAGTTGGACA
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81583 CAATCGGGTGGAAGAAGAGCCAGCACCGGGCCTCACTGGCCATCACAGTATCGTCTGACCTCTTCGACCGGGCCCGAAACGGGCGAACCGAG
81675 AGCGTTCCGCGCATCTGTCGGTCGGGCGTGTCGAAGGTGCGGCTGTTCGCCACGTGCGCGGCGAGCAGGGTGCCCTCCGCGCCGTCACGGGT
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81859 CGGCGGCCCTCCGCGCCGGACCGGGAACGCGGCACGCTCACCCCGCGTGATCCCTTGCCCACGAAGGGCTCGTCTGAATAGCATCAGCACAT
81951 CAGGCCCCACCATTACCCGGCACCATTGGCATTCGCTTTCTTCGACGTTGCGGCTGCGGTGCCCGGGCGTTGCATTTCCGGCGGAAAGGTGT
82043 TGCACGGTGCGTGAAACAAATGGCTCGACCGTGCCGCGACGGCAGCTCGGCAGGCTGCTCACCCAGCTCCGCGAGAGCGCCCATATCAGCA
> V P R R Q L G R L L T Q L R E S A H I S
82134 TCGACGCGGCGGCCGGCGAGCTGGACTGCTCGCGGCAGAAGCTCTGGCGGATCGAGCGGGGGCTGACCTCGGCCAAGACACCGGACGTCCGG
>I D A A A G E L D C S R Q K L W R I E R G L T S A K T P D V R
82226 GTGCTCTGCGAGCTGTACCGGGCCACGCCCGACCAGGCGAGCGTGCTGCTCGGGCTCGCCGAGGTGAGCCGGGCCGAGGGGTGGTGGCACGC
> V L C E L Y R A T P D Q A S V L L G L A E V S R A E G W W H A
82318 CCACGGCAGCTCCGTGCCGGCCTGGTTCTCGCTCTACGTCGGCCTGGAGAACGTCGCGAGCAGCATTCGGCACTACAACGCGGAGCTGGTGC
> H G S S V P A W F S L Y V G L E N V A S S I R H Y N A E L V
82410 CGGGGCTGTTGCAGACCCCCGGCTACGCCACCGCGCTCTTCGAGCACAACCGGCCCGAGCTGGGCGAGGAGGAGCGAAAGAAGGCGGTGGGC
>P G L L Q T P G Y A T A L F E H N R P E L G E E E R K K A V G
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> F R T Q R Q G L L A R R L P P A P E L T V I L S E A V L R R P
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> V P G R S V M A D Q L R H L L A V G E R H N I T V R V L P L
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> A L G A R Q S A E L I D A I R G E C Y E •
82961 CACCCGCAGCGGCACCAACGGCGGGGACTGCGTCGAGGTGGCCGACAACCTCACCGGCATCGTCGGCGTCCGGGACAGCAAGGACCCGGGCG
83053 GGCCGGCCCTGACCGTCCCGCCCGCCGCCTGGTCCGCCTTCGTCACCGAGGTCAAGGCCAACCGCCTCACCCGCTGACAGCTCCGCAACGAA
83145 CCAACCCCCGGCTACGCCTCAGACGCGGCCAGCGCCCCAGGGCTGCCCACGCCTCAGACAGCCCGCGCCTCAGACGTGCCTGCGCCTCAGAC

Figure 11U

```
83237 AGCCCGGGCCGCAGGGGCGCGTGCGCCTCAGACGGCCCGGGCCTCAGGCGCGCTTGCCGAGGGCGGCGTCGACCGCCTTGCCCAGGGCGGT
                                                    <  •  A  R  K  G  L  A  A  D  V  A  K  G  L  A  T
83328 GACGACCAGGGCCACCGAGGGGCGGACCACCGAGTCGTCCAGGCTGACGGTGCCGGAGAAGCCGGCCCCGCCCGCGATCTCCTCCAGCCGAC
      <  V  V  L  A  V  S  P  R  V  V  S  D  D  L  S  V  T  G  S  F  G  A  G  G  A  I  E  E  L  R  R
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      <  R  A  D  V  A  A  D  G  T  L  G  L  A  P  E  M  R  L  V  A  V  L  T  A  L  A  A  T  A  E
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      <D  P  I  Q  G  G  A  L  A  E  A  L  R  R  R  S  D  E  E  V  T  A  D  A  T  P  Y  R  H  V  H
83604 GATGAAGCCCAGCTCGGTCTCCTCGACGTCGCGCACCACGCCCCGGGCGACCAGGTCGCCGAGGATCCGGTCGCGCAGGCCGTGGCGCAGCC
      <  I  F  G  L  E  T  E  E  V  D  R  V  V  G  R  A  V  L  D  G  L  I  R  D  R  L  G  H  R  L  R
83696 GCTGCACCCAGGAGGACGGGGTGTGCGGCGTGTCGGCGGCCATCCGGCCCAGGACCTCGTCCAGGATCGGTTCGCCGGTGGGCGCGGGGTCC
      <  Q  V  W  S  S  P  T  H  P  T  D  A  A  M  R  G  L  V  E  D  L  I  P  E  G  T  P  A  P  D
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      <T  V  V  L  N  G  D  V  Y  A  V  R  G  A  L  A  L  E  I  L  V  A  A  A  M  G  L  D  L  S  I
83880 CCGCGGCATGGTCGCCTTGCCGGATTCGTCGTCGTACGCGAGGAGCAGCAATTCCTCGGCCAGCGCAACACCAGTCATGGCCGGAGACGG
      <  R  P  M
83970 TAGCGCCTGAGCGCACCCCGTGCGCCCCCAACTCGCCCACGAGCGCACTCGCCCGGTGAGAGGGGAACCCCGCTATACCGCAGGCGTTAACA
84062 GGGGGCCCTTCCTTGCGATCAGAAGCGGGGCATACCGCCGAACTGGCGGTCGCCGGCGTCGCCGAGGCCCGGCACGATGAACATCCGGTCG
                              <  •  F  R  P  M  G  G  F  Q  R  D  G  A  D  G  L  G  P  V  I  F  M  R  D
84153 TTGAGGCTCTCGTCGATCGCGGCGGTGACGAGGCGCAGCGGCAGGCCGGACTGCTCCAGCCGGGCGATGCCGACGGGCGCGGCGAGCACGCA
      <N  L  S  E  D  I  A  A  T  V  L  R  L  P  L  G  S  Q  E  L  R  A  I  G  V  P  A  A  L  V  C
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      <  L  V  T  I  D  T  C  G  R  E  A  L  L  R  C  C  H  E  L  S  G  G  T  A  L  M  P  D  L  V  L
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      <  T  G  E  A  D  T  V  P  T  Q  V  P  Y  K  E  V  P  F  S  R  A  A  E  Y  V  L  M  T  T  L  E
84613 CGTGCAGCGCGGCCCGGAAGTTGGAGGAGTCGGTGCGCGCGTCCCGCATGGCGGTCAGCCGCGACTGGGCGAGCGGATGGTCAATGACGTGT
      <  H  L  A  A  R  F  N  S  S  D  T  R  A  D  R  M
84705 ACGTCCACGATCGCCCAACCTACCGAACGCCCGGGCCCCGAGACACGAGGAGCGACGCCGCTCACCCGGCCCGTGCGGCAACCCTGGACGGT
84797 TGGCGTTCGAAGGTAGGGCAGGTGCCCAAGGTCGGGCCCGACCTCGCCGCGTGATCAAGATCACGAGGCGTGCGGGTGCGTAGACTTCCGGG
84889 CATGACGGCGACAGCGACGTCGGCCCGGTCGGACCTCTCCGAGCTGGGACGATCCGAGACCGCTTTGCGGAACTTCCTGCACGGCCTGCCG
      >  M  T  A  T  A  T  S  A  R  S  D  L  S  E  L  G  R  S  E  T  A  L  R  N  F  L  H  G  L  P
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      >  G  V  D  Q  V  G  A  E  Q  R  A  A  Q  L  G  T  R  S  I  K  T  T  A  K  A  R  A  I  D  L  A
85072 GATCCGGATGGTCGACCTGACCACCCTGGAGGGGGCCGACACCCCCGGCAAGGTGCGGGCGCTCGCGGCCCAAAGCACTGCGCCCCGACCCGG
      >  I  R  M  V  D  L  T  T  L  E  G  A  D  T  P  G  K  V  R  A  L  A  A  K  A  L  R  P  D  P
85164 CCGACCCGTCCTGCCCGCACGTCGGCGCAGTCTGCGTCTACCCGGCGATGGTCCCGTACGTGGCCGAGGTGCTGCGCGGATCCGCCGGGTCC
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85256 GGGCGGCCGTCCGGCGGACCGGACGGCAACGCGCCGGCCGGACCCGGCGTGGTGCACCTGGCCAGCGTGGCCACCGCGTTTCCGTCCGGGCA
      >  G  R  P  S  G  G  P  D  G  N  A  P  A  G  P  G  V  V  H  L  A  S  V  A  T  A  F  P  S  G  Q
85348 GGCACCCCTGGAGGTCAAGCTCGCCGACACCCGGGCCGCAGTGGCGGCTGGCGCGGACGAGATCGACATGGTGATCAACCGGGGCGCGTTCC
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85532 GAGCTGGCCACGTACGACAACGTGCGCCGCGCGTCCTGGCTGGCCATGCTGGCCGGCGGCGACTTCATCAAGACCTCGACGGGCAAGGTTCC
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85716 CCGGCGGCATCAAGAACACCAAGGACGCGATCAAGTACCTGGTTATGGTCAACGAGACCGTCGGCCCGGACTGGCTGGACCCGGACTGGTTC
      >A  G  G  I  K  N  T  K  D  A  I  K  Y  L  V  M  V  N  E  T  V  G  P  D  W  L  D  P  D  W  F
85808 CGGTTCGGCGCGTCCAGCCTGCTCAACGACCTGCTCATGCAGCGCACCAAGCTGACGACCGGCGTCTACTCCGGTCCCGACTACTTCACCCT
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85900 GGACTGAGCGTGATCTTCGAATACGCGCCCGCCCCCGAGTCCCGCTCGGTGGTGGACCTCAAGCCCTCGTACGGGCTGTTCGTCGACGG
      >  D  •  >  V  I  F  E  Y  A  P  A  P  E  S  R  S  V  V  D  L  K  P  S  Y  G  L  F  V  D  G
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      >  E  F  V  D  P  A  D  G  G  G  F  K  S  V  N  P  A  S  E  E  V  L  A  E  I  A  E  A  G  S
86081 CCGACGTGGACCGGGCGGTCCGCGCCGCCCCGGACGGCGTACGAGAAGGTGTGGGGCCCGATGCCGGGCCGGGACCGGGCCAAGTACCTGTTC
      >A  D  V  D  R  A  V  R  A  A  R  T  A  Y  E  K  V  W  G  P  M  P  G  R  D  R  A  K  Y  L  F
86173 CGGATCGCCCGGATCATCCAGGAGCGCTCCCGCGAGCTGGCCGTGCTGGAGTCCCTGGACAACGGCAAACCGATCCGGGAGTCCCGGGACGT
      >  R  I  A  R  I  I  Q  E  R  S  R  E  L  A  V  L  E  S  L  D  N  G  K  P  I  R  E  S  R  D  V
86265 CGACCTGCCGCTGGTCGCCGCGCACTTCTTCTACTACGCGGGCTGGGCAGACAAGCTGCCGTACGCGGGCTTCGGCCCGAACCCCCGGCCGC
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86357 TCGGCGTGGCCGCGCAGGTCATCCCGTGGAACTTCCCGCTGCTCATGCTCGCCTGGAAGATCGCCCCGGCGCTGGCCGCCGGCAACACGGTG
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86817 CGCCGAGCAGGTGCTGGAGTCGCTGAAGCGCCGAATGGCGCTGCTGCGGGTCGGCGACCCGTTGGACAAGAACACCGACATCGGGGCGATCA
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86909 ACTCGGCCGCCCAGCTCGCCCGCATCCGCGAGCTGTCCGCCGCGGGCGAGGCCGAGGGGGCGGAGCGCTGGTCGCCGCCGTCGAGCTGCCC
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87001 GAGCGCGGGTTCTGGTTCGCGCCGACGATCTTCACGGGGGTCACCCAGGCGCACCGGATCGCCCGGGAGGAGATCTTCGGTCCGGTGCTGTC
      >  E  R  G  F  W  F  A  P  T  I  F  T  G  V  T  Q  A  H  R  I  A  R  E  E  I  F  G  P  V  L  S
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Figure 11V

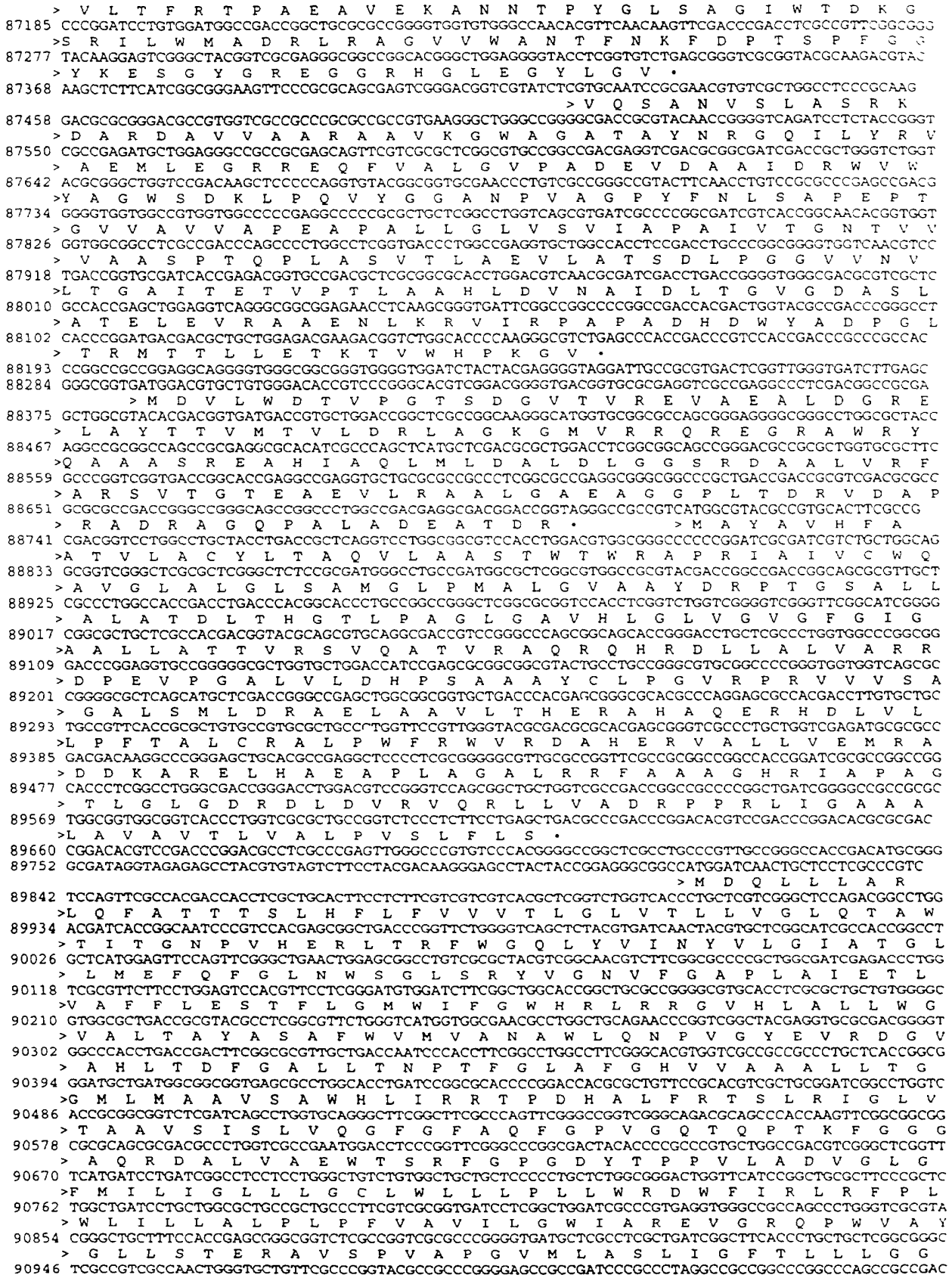

Figure 11W

Figure 11X

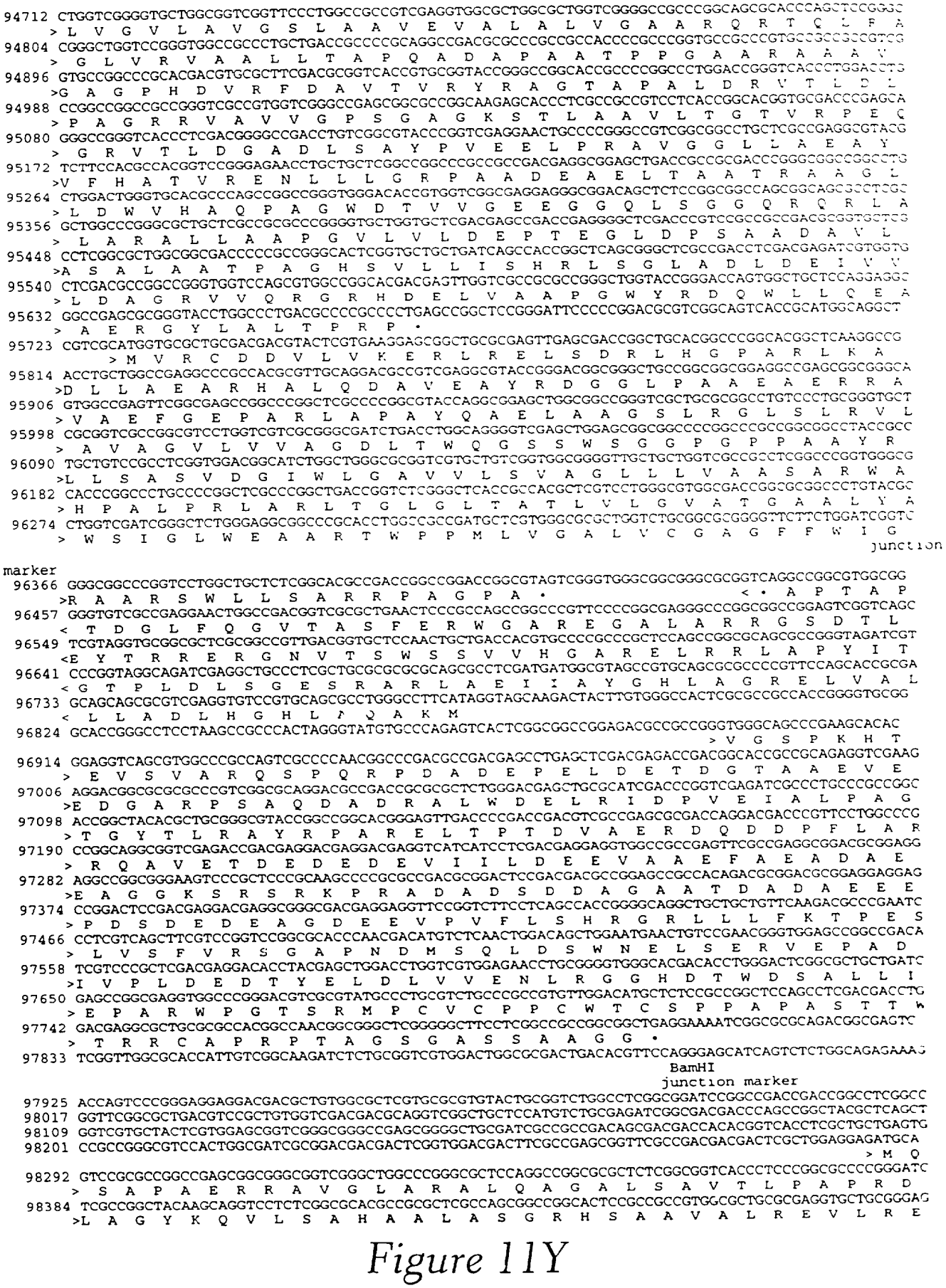

Figure 11Y

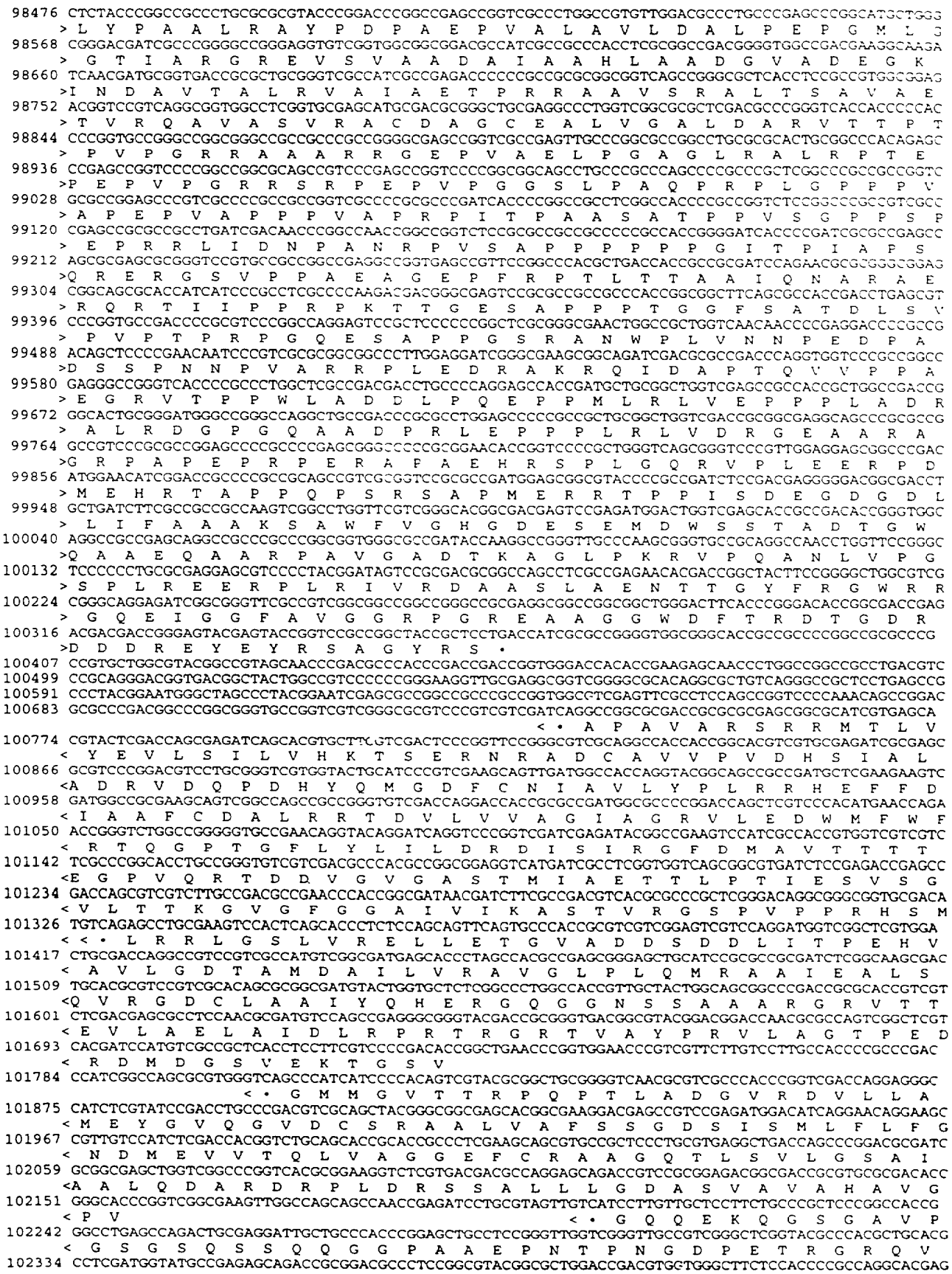

Figure 11Z

SUBSTITUTE SHEET (RULE 26)

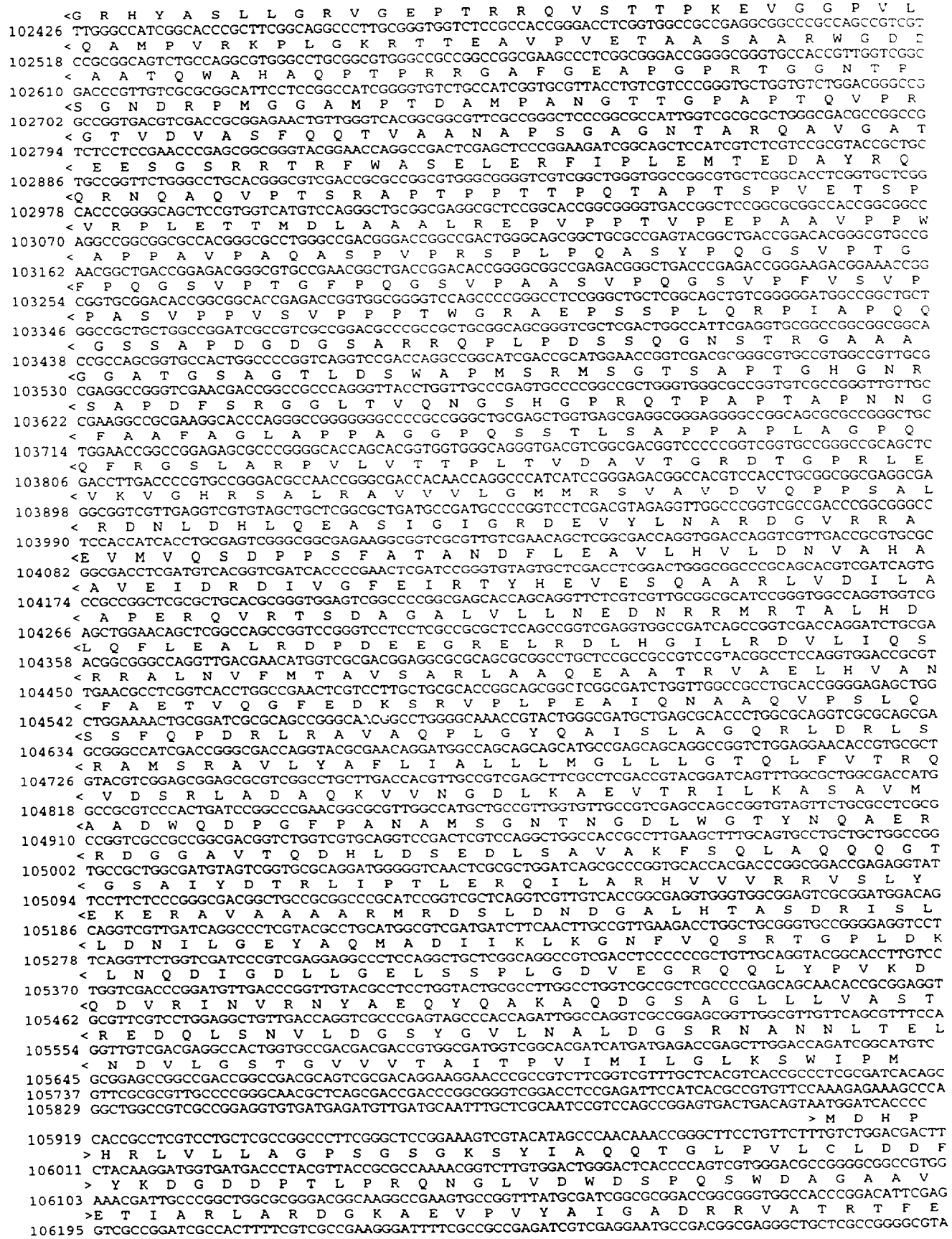

Figure 11AA

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      >V A G S P L F V A E G I F A A E I V E E C R R R G L L A G A Y
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      > A L R R P R G T T F F R R L A R D L A E Q R K A P G M L L R
106379 GCGGCCTGGCCCTGCTGCGCGCGGAGCCGGCGGTGCTGCGCCGCCAGGCGGGGCTCGGCGCTCACCCGGCCCCGGCCCGCGAGGTGCTGCGC
      >R G L A L L R A E P A V L R R Q A G L G A H P A P A R E V L R
106471 CGGGTGGCCGACCTGCTCGCCGGCCACCCGCACCACCCCTGATCAGCCCAGCAGCTTCCCGTACGCCGGCTTGATCACCTCGTCGATGAT
      > R V A D L L A G H P H H P • • G L L K G Y A P K I V E D I I
106561 GGCCAGCCGCTCGTCGAACGGGATGAACGCGCTCTTCATCGCGTTGATGGTGAACCATTGGAGCTCCTTCCAGCCGTAGCCGAAGGCCTCCG
      < A L R E D F P I F A S K M A N I T F W Q L E K W G Y G F A E A
106653 CCAGCAGCGCCATCTCCCGGGACATCGAGGTGCCGCTCATCAGCCGGTTGTCGGTGTTCACCGTCACCCGGAACCGCAGATCGCGCAGAAGC
      < L L A M E R S M S T G S M L R N D T N V T V R F R L D R L L
                                                          BamHI
                                                          junction marker
106745 CCGATCGGGTGCTCGGCGATCGACGCCGCCGCGCCGGTCTGCACGTTCGACGACGGGCACAGCTCCAGCGGGATCCGCTTGTCCCGCACGTA
      <G I P H E A I S A A A G T Q V N S S P C L E L P I R K D R V Y
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      < I A Q W I S P L G F A E G A H I T F H F N E R Q L Y E F A D
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107297 ACCCCGTCGGCGGCCAGGTCCAGCGCGCACTCCTGGGCCACCCGCCGCAGTGCGGGCGCGGTCTGCATGACCGCCACGGTGTGGGCGAACGT
      <V G D A A L D L A C E Q A V R R L A P A T Q M V A V T H A F T
107389 CTCCAGGTAGCGCTCCAGCGAGCCGGAGTTCGCCGCCGCGACGAACCAGCGGCCGAGCGCTTCCGGGTCGGTGGTGGGCAGCTCGTGGCCGA
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107846 GCGCCGACTTCCTCGCCGCCGGGCACTACGACACGCTCTCGGCCGCGCTCGCCGCCGCCGCGCTCGCCGCGCTGAGCCACCCGCCGGAGGCC
      >R A D F L A A G H Y D T L S A A L A A A A A L A A L S H P P E A
107938 CCCGGAGCGGACGCGTCGGCCGGCAAAGACGGGCAGGATGCCCAAGCCGGGCGGGATGCGTCCGCTGGACATGACGCGTCCGCCGGACAGCC
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108030 GGCCGTCGGGACGTACCCGCTGGTGGTGGACGCCGGGGCGGGCACGGGCCGGCACCTCGCCGCGGTGCTGGCGGCGCTGCCCGACGCCGTGG
      > A V G T Y P L V V D A G A G T G R H L A A V L A A L P D A V
108122 GCCTGGCCCTGGACGTCTCCAAGCCGGCGCTGCGCCGGGCAGCGCGGGCCCACCCGCGCGCGGCGGCGGCGCTCGCCGACACCTGGCGGCGG
      >G L A L D V S K P A L R R A A R A H P R A A A A A L A D T W R R
108214 CTTCCGCTGGCCGACGCCAGCGTCGCCGTGCTGCTCGACGTCTTCGCCCCCGCGCAACGGCGCGGAGTTCCGCCGGGTGCTCCACCCGGCCGG
      > L P L A D A S V A V L L D V F A P R N G A E F R R V L H P A G
108306 CGCGCTGCTCGTGGTCACCCCCGCCGAGGACCACCTCGCCGAACTGGTCGACTCGCTCGACCTGCTGAAGGTCGACCCCGACAAGGCGGACC
      > A L L V V T P A E D H L A E L V D S L D L L K V D P D K A D
108398 GGGTCGCCGGGAGCCTGGCCGGCCACTTCGAGCAGACCGCCGAGAGCGTGCTGCGGGCCCGGCTGGAACTCACCGGCCGGCAGGTGGCCACC
      >R V A G S L A G H F E Q T A E S V L R A R L E L T G R Q V A T
108490 CTGGTCGGGATGGGACCCAGCGCCTGGCACACCGACCCGGCCACCCTCGCCGCCCGGATCGCCGCGCTACCCGAGCCGGTCCGGGTGACCCT
      > L V G M G P S A W H T D P A T L A A R I A A L P E P V R V T L
108582 CGCGGTACGGCTCGGCGTGTACCGCCCCCGCTGACCGGGGCGCGGCCCGCCGCTCAGGTGGAAAGGTCGACCTCTTCCCAGCCCGGCGGCTC
      > A V R L G V Y R P R •                                    < • T S L D V E E W G P P E
108674 CTCGTGGTAGGGCCCTCGCAGGACCACCGCCCACTCCAGCGCCCACCGGCGCTGCCCGATCGCGTTGGCGTCGACCAGGCCGGGCGGCGACC
      < E H Y P G R L V V A W E L A W R R Q G I A N A D V L G P P S R
108766 GCCCGTCGCGCTCCAGCTCCAGGTACGCCCAGTCGAGGCAGTAGTGCAGGTCGAGCAGGGCCGCCGCGTCGGCCGGGTGCTGGGGCGCGGCC
      < G D R E L E L Y A W D L C Y H L D L L A A A D A P H Q P A A
108858 AGGATGCGGGAGCGCCACTGCTGGAAGCTCTCCCCGCCCGCGATGTGCGGCAGCCGCTCCACCAGCCGCTCGTCGACCGGCAGCGTCGGGTC
      <L I R S R W Q Q F S E G G A I H P L R E V L R E D V P L T P D
108950 GAGCTGCTTGGCCAGGCCGAGCACCCAGGCCAGCGAGAACAGCGCGTCGTGGTGCAGCACGAACGACCGGTGGTCGCCCCGGCCGCCCATCA
      < L Q K A L G L V W A L S F L A D H H L V F S R H D G R G G M V
109042 CGAACTGCCACTCCGGCGGGGTGACCAGGTCGACCAGGTGGGAGTTGAGCAGCCAGCTCATCGCCGCCTGCGCCGGCATGCCGAAACACCGG
      < F Q W E P P T V L D V L H S N L L W S M A A Q A P M G F C R
109134 GCCAGGATCACGTGCAGCACGGCGATGCGCGCCTCGATCTCGACGGTCGGCCGCAGCTCGATCTCGTCGCCCGGCTCCCACACCAGGGGAA
      <A L I V H L V A I R A E I E V T P R L E I E D G P E W V
109225 ACTGGCTCGGTGGCAGCGGCAGCCCCAGCCGGGACAGCTCGTCCAGGCTGGCGTCACGGACCTCTCTGCGGGTCGGGAGCGGAAACGCGCACG
109317 GCTCAGATCCCTGTCAGTCGCATCGGCTCAGTGCCGGTCGTCCCCCTTGGCCTGGGAGGATAGCGGTTCACGACGAGCGGCACCACGGCGGG
109409 CGGGGGCGGGGGCGGTTCAGCCGATCCGCTCGATGACCAGCGGCTGCGGGGTCGGGGCGGTCGGCGAGATCCGTACCGCCCGGACCGCCTCG
                  BamHI
109501 GCCAGCGCCGCCGGGATCC
```

Figure 11AB

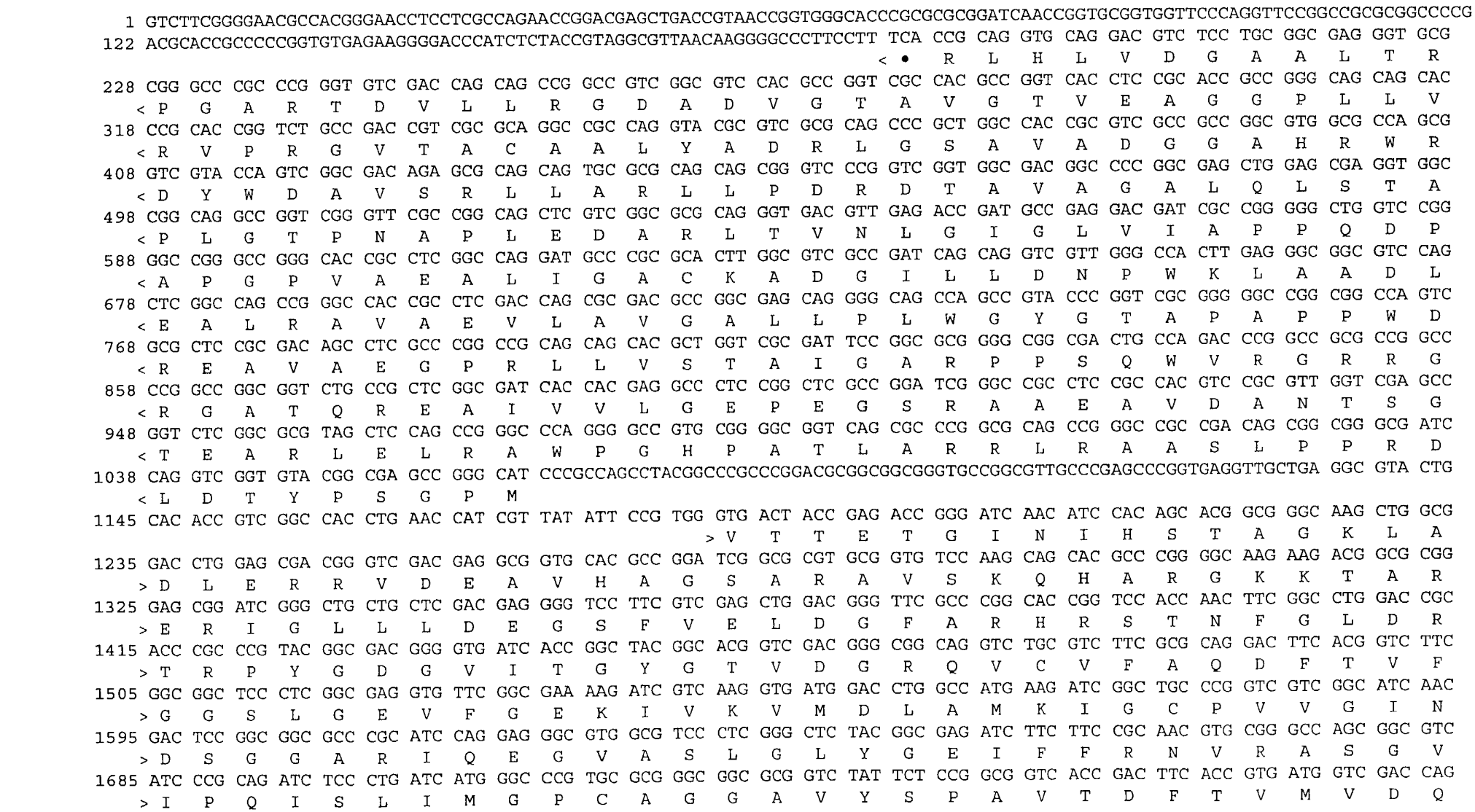
1 GTCTTCGGGGAACGCCACGGGAACCTCCTCGCCAGAACCGGACGAGCTGACCGTAACCGGTGGGCACCCGCGCGCGGATCAACCGGTGCGGTGGTTCCCAGGTTCCGGCCGCGCGGCCCCG
122 ACGCACCGCCCCCGGTGTGAGAAGGGGACCCATCTCTACCGTAGGCGTTAACAAGGGGCCCTTCCTT TCA CCG CAG GTG CAG GAC GTC TCC TGC GGC GAG GGT GCG
< • R L H L V D G A A L T R
228 CGG GCC CGC CCG GGT GTC GAC CAG CAG CCG GCC GTC GGC GTC CAC GCC GGT CGC CAC GCC GGT CAC CTC CGC ACC GCC GGG CAG CAG CAC
< P G A R T D V L L R G D A D V G T A V G T V E A G G P L L V
318 CCG CAC CGG TCT GCC GAC CGT CGC GCA GGC CGC CAG GTA CGC GTC GCG CAG CCC GCT GGC CAC CGC GTC GCC GCC GGC GTG GCG CCA GCG
< R V P R G V T A C A A L Y A D R L G S A V A D G G A H R W R
408 GTC GTA CCA GTC GGC GAC AGA GCG CAG CAG TGC GCG CAG CAG CGG GTC CCG GTC GGT GGC GAC GGC CCC GGC GAG CTG GAG CGA GGT GGC
< D Y W D A V S R L L A R L L P D R D T A V A G A L Q L S T A
498 CGG CAG GCC GGT CGG GTT CGC CGG CAG CTC GTC GGC GCG CAG GGT GAC GTT GAG ACC GAT GCC GAG GAC GAT CGC CGG GGG CTG GTC CGG
< P L G T P N A P L E D A R L T V N L G I G L V I A P P Q D P
588 GGC CGG GCC GGG CAC CGC CTC GGC CAG GAT GCC CGC GCA CTT GGC GTC GCC GAT CAG CAG GTC GTT GGG CCA CTT GAG GGC GGC GTC CAG
< A P G P V A E A L I G A C K A D G I L L D N P W K L A A D L
678 CTC GGC CAG CCG GGC CAC CGC CTC GAC CAG CGC GAC GCC GGC GAG CAG GGG CAG CCA GCC GTA CCC GGT CGC GGG GGC CGG CGG CCA GTC
< E A L R A V A E V L A V G A L L P L W G Y G T A P A P P W D
768 GCG CTC CGC GAC AGC CTC GCC CGG CCG CAG CAG CAC GCT GGT CGC GAT TCC GGC GCG GGG CGG CGA CTG CCA GAC CCG GCC GCG CCG GCC
< R E A V A E G P R L L V S T A I G A R P P S Q W V R G R R G
858 CCG GCC GGC GGT CTG CCG CTC GGC GAT CAC CAC GAG GCC CTC CGG CTC GCC GGA TCG GGC CGC CTC CGC CAC GTC CGC GTT GGT CGA GCC
< R G A T Q R E A I V V L G E P E G S R A A E A V D A N T S G
948 GGT CTC GGC GCG TAG CTC CAG CCG GGC CCA GGG GCC GTG CGG GGC GGT CAG CGC CCG GCG CAG CCG GGC CGC CGA CAG CGG CGG GCG ATC
< T E A R L E L R A W P G H P A T L A R R L R A A S L P P R D
1038 CAG GTC GGT GTA CGG CGA GCC GGG CAT CCCGCCAGCCTACGGCCCGCCCGGACGCGGCGGCGGGTGCCGGCGTTGCCCGAGCCCGGTGAGGTTGCTGA GGC GTA CTG
< L D T Y P S G P M
1145 CAC ACC GTC GGC CAC CTG AAC CAT CGT TAT ATT CCG TGG GTG ACT ACC GAG ACC GGG ATC AAC ATC CAC AGC ACG GCG GGC AAG CTG GCG
> V T T E T G I N I H S T A G K L A
1235 GAC CTG GAG CGA CGG GTC GAC GAG GCG GTG CAC GCC GGA TCG GCG CGT GCG GTG TCC AAG CAG CAC GCC CGG GGC AAG AAG ACG GCG CGG
> D L E R R V D E A V H A G S A R A V S K Q H A R G K K T A R
1325 GAG CGG ATC GGG CTG CTG CTC GAC GAG GGG TCC TTC GTC GAG CTG GAC GGG TTC GCC CGG CAC CGG TCC ACC AAC TTC GGC CTG GAC CGC
> E R I G L L L D E G S F V E L D G F A R H R S T N F G L D R
1415 ACC CGC CCG TAC GGC GAC GGG GTG ATC ACC GGC TAC GGC ACG GTC GAC GGG CGG CAG GTC TGC GTC TTC GCG CAG GAC TTC ACG GTC TTC
> T R P Y G D G V I T G Y G T V D G R Q V C V F A Q D F T V F
1505 GGC GGC TCC CTC GGC GAG GTG TTC GGC GAA AAG ATC GTC AAG GTG ATG GAC CTG GCC ATG AAG ATC GGC TGC CCG GTC GTC GGC ATC AAC
> G G S L G E V F G E K I V K V M D L A M K I G C P V V G I N
1595 GAC TCC GGC GGC GCC CGC ATC CAG GAG GGC GTG GCG TCC CTC GGG CTC TAC GGC GAG ATC TTC TTC CGC AAC GTG CGG GCC AGC GGC GTC
> D S G G A R I Q E G V A S L G L Y G E I F F R N V R A S G V
1685 ATC CCG CAG ATC TCC CTG ATC ATG GGC CCG TGC GCG GGC GGC GCG GTC TAT TCT CCG GCG GTC ACC GAC TTC ACC GTG ATG GTC GAC CAG
> I P Q I S L I M G P C A G G A V Y S P A V T D F T V M V D Q

FIGURE 12A

```
1775 ACC TCG CAC ATG TTC ATC ACC GGC CCC GAC GTG ATC AAG ACG GTC ACC GGC GAG GAC GTC GGG ATG GAG GAA CTG GGC GGT GCC CGC ACC
    > T   S   H   M   F   I   T   G   P   D   V   I   K   T   V   T   G   E   D   V   G   M   E   E   L   G   G   A   R   T
1865 CAC AAC GCG CGC AGC GGC AAC GCG CAC TAC CTC GGC ACC GAC GAG GAG GAC GCG ATC GAG TAC GTC AAG GCG CTG CTG TCG TAC CTG CCG
    > H   N   A   R   S   G   N   A   H   Y   L   G   T   D   E   E   D   A   I   E   Y   V   K   A   L   L   S   Y   L   P
1955 TCG AAC AAC CTG GAC GAG CCG CCG GTC TTC GAC GCC CCG GCC GAC GTG GCG ATC AGC GAC GCC GAC CGG GAG CTG GAC AGC CTC GTC CCG
    > S   N   N   L   D   E   P   P   V   F   D   A   P   A   D   V   A   I   S   D   A   D   R   E   L   D   S   L   V   P
2045 GAC TCG GCG AAC CAG CCG TAC GAC ATG CAC CGG GTC ATC GAG CAC GTG CTG GAC GAC GGG GAG TTC CTG GAG GTC CAG CCG CTG TAC GCG
    > D   S   A   N   Q   P   Y   D   M   H   R   V   I   E   H   V   L   D   D   G   E   F   L   E   V   Q   P   L   Y   A
2135 CAG AAC ATG GTG GTC GGC TTC GGT CGA ATC GAG GGA CGA CCG GTC GGC GTG GTG GCC AAC CAG CCG ATG CAC CTC GCC GGC ACG CTG GAC
    > Q   N   M   V   V   G   F   G   R   I   E   G   R   P   V   G   V   V   A   N   Q   P   M   H   L   A   G   T   L   D
2225 ATC GCC GCG TCG GAG AAG GCC GCC CGG TTC GTG CGC ACC TGC GAC GCG TTC AAC ATC CCC GTG CTG ACC TTC GTG GAC GTG CCC GGG TTC
    > I   A   A   S   E   K   A   A   R   F   V   R   T   C   D   A   F   N   I   P   V   L   T   F   V   D   V   P   G   F
2315 CTA CCC GGC ACC GGC CAG GAG TGG GAC GGC ATC ATC CGG CGC GGC GCG AAG CTC ATC TAC GCG TAC GCC GAG GCG ACC GTC CCG AAG GTC
    > L   P   G   T   G   Q   E   W   D   G   I   I   R   R   G   A   K   L   I   Y   A   Y   A   E   A   T   V   P   K   V
2405 ACC GTG ATC ACC CGC AAG GCG TAC GGC GGG GCG TAC GAC GTG ATG GGC TCC AAG CAC CTG GGC GCG GAT CTG AAC TTC GCC TGG CCG ACC
    > T   V   I   T   R   K   A   Y   G   G   A   Y   D   V   M   G   S   K   H   L   G   A   D   L   N   F   A   W   P   T
2495 GCG CAG ATC GCG GTG ATG GGC GCG CAG GGC GCG GTG AAC ATC CTG TAC CGG CAG GAG CTG GCC GCC GCC GAG GAC CCG GCC GCC GTG CGC
    > A   Q   I   A   V   M   G   A   Q   G   A   V   N   I   L   Y   R   Q   E   L   A   A   A   E   D   P   A   A   V   R
2585 GCC GAG AAG ATC GCC GAG TAC GAG GAC ACC CTG GCC AAC CCG TAC GTC GCC GCC GAG CGC GGG TAC GTC GAC TCG GTG ATC CCG CCG CAC
    > A   E   K   I   A   E   Y   E   D   T   L   A   N   P   Y   V   A   A   E   R   G   Y   V   D   S   V   I   P   P   H
2675 GAG ACG CGT ACC CAG ATC GTC CGG GCG TTG CGG GTG CTG CGC ACC AAG CGC GAG ACG CTC CCG GCG AAG AAG CAC GGC AAC ATC CCG CTC
    > E   T   R   T   Q   I   V   R   A   L   R   V   L   R   T   K   R   E   T   L   P   A   K   K   H   G   N   I   P   L
2765 TAG GCGCGGTGCAGGGAGGGGCCCCTGTCACGCGATCCGTGCAGCAGGGCCCCCTCCCGACGCCGGAGGAGCCGGCGGGCCCGGCAGCCGGGCGCCGG TCA GCA CGC CGG GTT
    > •                                                                                                                 < •   C   A   P   N
2878 GGC GGC GAG GCA CAT CCG CCG GGC GGC CGT GCG GCC CAG TTC GAG CAG CTC CGC GTC GCT GGT CTC GCG GGG GCC GTC CGG CCC GTC GAC
    < A   A   L   C   M   R   R   A   A   T   R   G   L   E   L   L   E   A   D   S   T   E   R   P   G   D   P   G   D   V
2968 GCC CAA CCC GCG CTC GGG CAC GAT GAC GGT GAC CAG GTC GCC GAC CCG GAC GAT CAT CCG GGT TTC CGG CGG GTA CCC CAC GTC GAG GGG
    < G   L   G   R   E   P   V   I   V   T   V   L   D   G   V   R   V   I   M   R   T   E   P   P   Y   G   V   D   L   P
3058 CTT GCC CGT CGT GGG GTC CAC CGG GGA CAT CAC GGT GTG CCG CAA CAC GAC CGC CTC GTC GCC GGC GAA GTC GCG GGC GAT CGT CTG CCA
    < K   G   T   T   P   D   V   P   S   M   V   T   H   R   L   V   V   A   E   D   G   A   F   D   R   A   I   T   Q   W
3148 GGT GTG GGC CAC CGA GAT CGC GCC ACG GCC GTC GTC CAG GGG CCG AAC CGC CGT GTC GCT CCA GCG GGC GCA GGT GGT CGC CGC CCG GTC
    < T   H   A   V   S   I   A   G   R   G   D   D   L   P   R   V   A   T   D   S   W   R   A   C   T   T   A   A   R   D
3238 CAG GTC GGC GAG CAG CCG GCC GGC CGG GGC GGG GTC GAG GCG GTA GAC GTC CTG GGT GAG GAC GGG GAC GGC CAT CGA CCC GTC CTG GCC
    < L   D   A   L   L   R   G   A   P   A   P   D   L   R   Y   V   D   Q   T   L   V   P   V   A   M   S   G   D   Q   G
3328 CGA CGT GTC GTC CAG GAG CAG CGT CTG GGA TCG CGA GTA GCG AGA CAC CGG CGG CCC CGC CCC CGG CTC CTT GCC CAC GGC GCA CGA CTG
    < S   T   D   D   L   L   L   T   Q   S   R   S   Y   R   S   V   P   P   G   A   G   P   E   K   G   V   A   C   S   Q
3418 GAG CAG CGG GTC CAC CCG GAC CTG CTC CTG AAG CCC AGA GTC CCC CAG TCG TAC GTT GCT CGG CAC GCC CAG GTC GGC CGG GTC CAG CAG
    < L   L   P   D   V   R   V   Q   E   Q   L   G   S   D   G   L   R   V   N   S   P   V   G   L   D   A   P   D   L   L
```

FIGURE 12B

```
3508 GGC CTC CTG GCC GAT CTC GGT CCG GCC GGA CCG CTC CGG CTC GGT AGA CGC GCG CCA CCC GTC GAC CCA GGA CAT CGG CGG CGC GAG GTG
    < A   E   Q   G   I   E   T   R   G   S   R   E   P   E   T   S   A   R   W   G   D   V   W   S   M   P   P   A   L   H
3598 CCC GCC GGC CCG GCC GCC GAC CGC CAC GGC GAA GAC CGA GAG TAC GGC CAG CAC GGC CGC GGC CGC CGC CAT CGC CGT ACG CCG GCT GCG
    < G   G   A   R   G   G   V   A   V   A   F   V   S   L   V   A   L   V   A   A   A   A   A   M   A   T   R   R   S   R
3688 GCG GCG GGC CCG GGC GCG GAT GTC CGC CGG CTC GGG CCA ACG GAC GTC CCG CAG GTC CCG GTG CAT CCGTTCGGCGAACGTCAGGTCG TCA CGC
    < R   R   A   R   A   R   I   D   A   P   E   P   W   R   V   D   R   L   D   R   H   M                                   <   •   A
3782 ATC GGC GGC CTC CTC CAG GTC AGA GAC GGC GAG CAG CCC GGC GAG CGC GGC ACG CCC CCG GGA GAG ACG GGC TTT CAC GGT GCC GAC CGG
    < D   A   A   E   E   L   D   S   V   A   L   L   G   A   L   A   A   R   G   R   S   L   R   A   K   V   T   G   V   P
3872 GGC GGC GGT CTC CCG TGC CAC CTC GGC CAC CGG CAT GCC GAG CAG GTA GTG CAG GGC GAT GGC GGT GCG CTG CGC CTC GGG CAG CCG GCG
    < A   A   T   E   R   A   V   E   A   V   P   M   G   L   L   Y   H   L   A   I   A   T   R   Q   A   E   P   L   R   R
3962 TAG CGC CGC CAC CAC CTC CAG CGT CGC GGT GCT CGG CGC GGG GAC GCT CTC CGG CGC ACC GTG CCG CAG GTA CGC CCG CGC CCG GCT ACG
    < L   A   A   V   V   E   L   T   A   T   S   P   A   P   V   S   E   P   A   G   H   R   L   Y   A   R   A   R   S   R
4052 CAT GCT GCG CCA CCG GCT CAC CGC GAT CCG GCT CGC CAC CAC GCG CAG CCA GCC CTC CGG ATC GTC GTA CCC GCG TAC GGT CGG CCA GCG
    < M   S   R   W   R   S   V   A   I   R   S   A   V   V   R   L   W   G   E   P   D   D   Y   G   R   V   T   P   W   R
4142 CTG CCA TGC GCG GAT GTA CGC CTC CTG CAC GGC GTC CTG CGC CTC GGC CAG GTT TCC GGT GAT CAT GTA CAC GAA ACC CAG CAA TCG TTG
    < Q   W   A   R   I   Y   A   E   Q   V   A   D   Q   A   E   A   L   N   G   T   I   M   Y   V   F   G   L   L   R   Q
4232 CCG GCT GCC CCG GTA GAA CTC GTC GAA CCC CTC GGC GTC CGG CAT CCGCCACCTCCCCGTGTCGCAGGGGACACGCCTGGCGGGTGGTCCCCGGTTGCCCGACCGG
    < R   S   G   R   Y   F   E   D   F   G   E   A   D   P   M
4338 CCGGCTTCTTCCCTCCCCGGGGGTCCCCGGCGGGTTCCTCCCGGGGTCTCCCGGCGGGCCCGTCACGTCACGGCCGGCGCGGCGGGCTCGTCACGTCACGGCCGGCGCGGCGGGCCTTCGG
4459 CAGCGAACAGCGACCGTCCGAGAATCGGGTGCCGGCCGGAGTGGTCGAGGGCGCGGGTGGGCGGTGG TCA GAC CGT GAG CCC GGC GTC GGT GAG GAT CGG GCC GGC
                                                                                                    <   •   V   T   L   G   A   D   T   L   I   P   G   A
4565 GAG CAG CAG GGC GCC GAC GGC GAG GCC GGC CAG GCA GAC GAC CAG GAA GAC ACC GAC CCA GAA CAG GGG CGG GAA CGG CGT CAA CCG GGC
    < L   L   L   A   G   V   A   L   G   A   L   C   V   V   L   F   V   G   V   W   F   L   P   P   F   P   T   L   R   A
4655 GAG CTG GTC GGC GTC GGA CTC CGG CAT CCG GCC ACG GCT GCG CAG CCG CTG CAA CTC GAT CAC CGG ACG CAC GCC GCC GAA CAG CAG GAA
    < L   Q   D   A   D   S   E   P   M   R   G   R   S   R   L   R   Q   L   E   I   V   P   R   V   G   G   F   L   L   F
4745 CCA GAC CGA GGT CCA GGC GAA CGC GGC CTG CAC CTG CGG CGG GGC GTA CCA GGA GAC GGC GAA GAC CAG ACC GCC GGT GGC GAG CAG CGA
    < W   V   S   T   W   A   F   A   A   Q   V   Q   P   P   A   Y   W   S   V   A   F   V   L   G   G   T   A   L   L   S
4835 CAG TGC CCC GTA GAC GTT GCG GAT CAT CGC CAG CAT GGC CAG CAG CAG CAC CAC CGT GAC CGA GAG CAG CAT GGT GAT CCG GTT CCC GGC
    < L   A   G   Y   V   N   R   I   M   A   L   M   A   L   L   L   V   V   T   V   S   L   L   M   T   I   R   N   G   A
4925 GAG CAG CCA CGC CCC GGC CAG CCC GAG CAG GGT CGG GGC GAC GTA CCC GGC GAA CAG GGT GAG GAT CAT GCC CAG CCC GGT GGG GCG GCC
    < L   L   W   A   G   A   L   G   L   L   T   P   A   V   Y   G   A   F   L   T   L   I   M   G   L   G   T   P   R   G
5015 GGC CGA CAG GGT GAG CCC GGA GGT GTC CGA GTG CAG CCG GAT GCC GCG CAG CTT CCG CCC GGT GAG CAG GGC GGC CAG CGC ATG ACC GCC
    < A   S   L   T   L   G   S   T   D   S   H   L   R   I   G   R   L   K   R   G   T   L   L   A   A   L   A   H   G   G
5105 CTC GTG GGC GAT GGT CAC CGC GTT ACG CGC GAC CCG CCA GGG CAC CCG GGT GGC GAC CAC CGC CAG CGC GAC GGC GGC GGT GGC CAG GAC
    < E   H   A   I   T   V   A   N   R   A   V   R   W   P   V   R   T   A   V   V   A   L   A   V   A   A   T   A   L   V
5195 CAG CAG CGG TGG CGG GTC GGG TTG CGC GCC GAC GAG TTC GTT CCA GAC GAC GCT CAG GCC GTC GAT CAG GTC CAC GGG GCC GCA GCC TAG
    < L   L   P   P   P   D   P   Q   A   G   V   L   E   N   W   V   V   S   L   G   D   I   L   D   V   P   G   C   G   L
```

FIGURE 12C

```
5285 CGG CCC CGG CCC GGT TCG CGC GCC GCG CGC CCG CCA CGG CCG CGG TGC CCG GCC CGG GCC CGG TCG ACC AGC GCC GGG GCG CAC GCCCGCCGC
    < P   G   P   G   T   R   A   G   R   A   R   W   P   R   P   A   R   G   P   G   P   R   G   A   G   P   R   V
5378 TGACCGGCACCCGG TCA GGT CGC GGG CAC CCC GGT CAG GTC GCC TGC GAC GAA GAA GGC CGC CGC TCT GGT GCC CAC CCG CAA CCG CCG CCG
                   < •   T   A   P   V   G   T   L   D   G   A   V   F   F   A   A   A   R   T   G   V   R   L   R   R   R
5470 AGG GCG GAC CTC ACC GAC CGG CGG CAC CTT GCG TCC ACG TAG GAC CAC GGC GAG CAC CCC GGT CGG CGG CAG CAC GGA AGC GAC CCT GGT
    < P   R   V   E   G   V   P   P   V   K   R   G   R   L   V   V   A   L   V   G   T   P   P   L   V   S   A   V   R   T
5560 CAG CAT CCC GGG CAG GCC CTC CCC GGC CCG CTC CCC CTG CCA GCT CGT CTG CTC CCC GTA CGG CAG GTC GGT CAC GAC CAG GTC GGG GGT
    < L   M   G   P   L   G   E   G   A   R   E   G   Q   W   S   T   Q   E   G   Y   P   L   D   T   V   V   L   D   P   T
5650 CAT GCC CGC GAC GGC CTC GGT GAG GGC CAC GCG GTC GAA CAC GTC GGC CCG CCG CAC CGC GTA CGG CAG CGG GCC GCC TGC CGC GTC CAG
    < M   G   A   V   A   E   T   L   A   V   R   D   F   V   D   A   R   R   V   A   Y   P   L   P   G   G   A   A   D   L
5740 ACG GGC GCG CAG CCG GTG GGC GGC GGC GGC CGC CTC CGC GTA GTG CGG CTT GTC GAA CGC CTC GGC GCG TTG CGC CAG CTC GCG GGC CCG
    < R   A   R   L   R   H   A   A   A   A   A   E   A   Y   H   P   K   D   F   A   E   A   R   Q   A   L   E   R   A   R
5830 CGT GTC GAG CCC GGC GCC GGT CAG CAG GCC GAG GTT GGC CCG AGC AAG GTC GAG GGC CGC CTC GTC GAC GTC GGA GGC GAG CAG CCC GGC
    < T   D   L   G   A   G   T   L   L   G   L   N   A   R   A   L   D   L   A   A   E   D   V   D   S   A   L   L   G   A
5920 AAG GCT CGG CCG GTG CAG CAG CGC GAG CAC CGT CAG CAG GTA GCC GCT GCC GCA GCA CGG GTC CCA GAC GGT GGC CGG GGC GGA CGT CGG
    < L   S   P   R   H   L   L   A   L   V   T   L   L   Y   G   S   G   C   C   P   D   W   V   T   A   P   A   S   T   P
6010 GCG CAA CTC CAG CGC GGT TTG CAG GAC CTC GGA GGC GAG CCG CAC CGG GAA CGC CGG GAA GCC CGG CGC CGA GCG CAA CAC GGC GCC ACT
    < R   L   E   L   A   T   Q   L   V   E   S   A   L   R   V   P   F   A   P   F   G   P   A   S   R   L   V   A   G   S
6100 GGC CAG GTC GCC GTA CGC ACC GCG TAC GGT TTC GTG CCG GTA AGT CAC ATG CCC TCC CCG GCG CAC CCT ACC AAT CCG GCA CCG CCG GGC
    < A   L   D   G   Y   A   G   R   V   T   E   H   R   Y   T   V
6190 CGG G TCA GGC AGG CCG GGA CTC GAT CCA GTG GAA GTC GGT GGG AGG CAG CGG CGT GAC GTC CTC CAG GGA CAG CCC CGC CTT GCC GCA CAG
            < •   A   P   R   S   E   I   W   H   F   D   T   P   P   L   P   T   V   D   E   L   S   L   G   A   K   G   C   L
6281 CCG TTC CAG GTC GCC TCG GGT CCG CTC CAG GCC CTG CCC GTT GAC CAG CAT CCC CAC GTC GGT CAG GTA CGC CAG CGC GTT GGC CGC CGG
    < R   E   L   D   G   R   T   R   E   L   G   Q   G   N   V   L   M   G   V   D   T   L   Y   A   L   A   N   A   A   P
6371 GCC GAC CAC GTC CGG CAG CAC GTG GTC GAT CAT GAC GAT CCG GCC GCC CGG GGC GAC CGC CTC GGC ACA GTG CCG GAG GAT TCC CGT CGC
    < G   V   V   D   P   L   V   H   D   I   M   V   I   R   G   G   P   A   V   A   E   A   C   H   R   L   I   G   T   A
6461 CCG GCC GTC GCC CCA ACC GTG GAT CAC ACT TTT GAG CAG GTA GAG GTC GGC GTC GGC GGG GAC CCT CTC GAA GAA GTC ACC CAC CTC GAT
    < R   G   D   G   W   G   H   I   V   S   K   L   L   Y   L   D   A   D   A   P   V   R   E   F   F   D   G   V   E   I
6551 CCG GCA CCG GTC GCC GAC CCC GGC GCG GCG CAG GTT CCC CGC CGC CTC CGC GCT GCC GCT GGC GCT GTC GTA GAG CAC GCC CCG CAC GCC
    < R   C   R   D   G   V   G   A   R   R   L   N   G   A   A   E   A   S   G   S   A   S   D   Y   L   V   G   R   V   G
6641 GGG GTT CGC GGC GAG CAC GGC GGC CAG CAG GGT GCC GTC TCC GCC GCC CAC GTC GAC CAC CGT CCG CAC GCC GGC CAG GTC GGT ACG CTC
    < P   N   A   A   L   V   A   A   L   L   T   G   D   G   G   G   V   D   V   V   T   R   V   G   A   L   D   T   R   E
6731 GGC AAC GGC CGC CGC GAC GCT GTG GGT CAC CTG GCT CAT CGC CGC GTT GTA CAG CTC GGA AAG GTC GGG TCG CCC GCC CAC GTA GCT GAA
    < A   V   A   A   A   V   S   H   T   V   Q   S   M   A   A   N   Y   L   E   S   L   D   P   R   G   G   V   Y   S   F
6821 GAA GTC GGT GCC GAA GAT GCC GTC GAA GGC CGG CTC GCC GGT GCG GAC GCT GTG CGC CAG GCC GTC CCA GGC CGT GGT CAT GGC CGG GTC
    < F   D   T   G   F   I   G   D   F   A   P   E   G   T   R   V   S   H   A   L   G   D   W   A   T   T   M   A   P   D
6911 GGT CAG CAT CCG GGC CAG CGG GCG CAG CGT GCC GGG TCG GTC CCC ACG CAG CAG CGC CCC CAT CGG GGC GAG CGC GAA CCG GCC GGG TGT
    < T   L   M   R   A   L   P   R   L   T   G   P   R   D   G   R   L   L   A   G   M   P   A   L   A   F   R   G   P   T
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FIGURE 12D

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7001 GGT CTC GGT GAG CAC CCG CAG CGC GGC CAG GGC GCG CAG CAC CCG GAA CAT GGT GTC CGC TCG GGC GTC GTA CCG CAG CGC CAA CTC CTG
    < T   E   T   L   V   R   L   A   A   L   A   R   L   V   R   F   M   T   D   A   R   A   D   Y   R   L   A   L   E   Q
7091 CGG GGT GCG CTC GTC GTC GCC GAT CGC GTC GGG CAG CCC CAG CCG GAC GCA GTA GCC GAC CAG CCG GCT GGC CAT CCC GCC GAA CAC CAA
    < P   T   R   E   D   D   G   I   A   D   P   L   G   L   R   V   C   Y   G   V   L   R   S   A   M   G   G   F   V   L
7181 CCG CAT CAG CTC CGG CCA GGC GGC GTC CGC GCC GGT CTG CGC CCG GCG GGC GCT GGG CTC GTC GGT CGT CGT GGC CC GCTCGTCCGTGTCCGGGA
    < R   M   L   E   P   W   A   A   D   A   G   T   Q   A   R   R   A   S   P   E   D   T   T   T   A   R   E   D   T   D   P   V
7276 CGG TCA TCG GAC CGG CTC GGC GGC CGG CAG GCC CAG CCC GAT GCG CAC GGC CCG TTC GAC CGG CGA GTA GTC GCC GTC CGG GCG GTC CAG
    < T   M
        <   R   V   P   E   A   A   P   L   G   L   G   I   R   V   A   R   E   V   P   S   Y   D   G   D   P   R   D   L
7366 GTC CAG CTC GCC CAC CGG CTG CAG GCT CGG CTG GGC CAT GAA CCG GGG CCG CGT GCC GGT GTT GGC CAC CGG GGT GTG CAC CAG GAA CGG
    < D   L   E   G   V   P   Q   L   S   P   Q   A   M   F   R   P   R   T   G   T   N   A   V   P   T   H   V   L   F   P
7456 GTG GCA CAG GTA GAC GTC ACC GGC GCG TCC GGT GGC GGA GGC GAG CGG GCG GTC CCG GCC GAC GTC GCC CAC GTC GAG GTA GGT GCC CTC
    < H   C   L   Y   V   D   G   A   R   G   T   A   S   A   L   P   R   D   R   G   V   D   G   V   D   L   Y   T   G   E
7546 CGG GCC GTA CGG TTC GAG CAG CGG CGG CAC GTC CAG GTG GGA GCC GAC CCT GAC CAG CGT CGG CGC CTC CCG CTC GTC GGT GTC GGA GAA
    < P   G   Y   P   E   L   L   P   P   V   D   L   H   S   G   V   R   V   L   T   P   A   E   R   E   D   T   D   S   F
7636 GAG GAA CAG CAG CAG CAG GGC CCG CCC CCG CGA CCG GAG GTT GCA GCG GAA GAC CTC CGC GTA GTT GGG CGG GAC CAG GTC CAG CTC GCC
    < L   F   L   L   L   L   A   R   G   R   S   R   L   N   C   R   F   V   E   A   Y   N   P   P   V   L   D   L   E   G
7726 CTC CCA GTT CTG GGG GCC CAG CCG CTG CGC GTC GTC GGC CAG GAA ACT GGC GTC GAT GTG CCA GCC GTA GTC CTC GGT CTG CTC CGG GCG
    < E   W   N   Q   P   G   L   R   Q   A   D   D   A   L   F   S   A   D   I   H   W   G   Y   D   E   T   Q   E   P   R
7816 CTT GGG CAC CGG GAA CCG GAC CGG GAA GGT GCC GAT CCG GTC CAA CGG CTT CCA GCG CCC CAC CCC GAC GAG CTG GTC GAA GGC GGC GTG
    < K   P   V   P   F   R   V   P   F   T   G   I   R   D   L   P   K   W   R   G   V   G   V   L   Q   D   F   A   A   H
7906 CAG CCG GGG CGT GGT GGC GCT GCG CAC GAA GGG CTC GGC GTC CTG GAG GCC CAG CCG GAC CAC CTC GCG GGA CCA GGT GCT CCG GTC CTC
    < L   R   P   T   T   A   S   R   V   F   P   E   A   D   Q   L   G   L   R   V   V   E   R   S   W   T   S   R   D   E
7996 GGG GTC CAT GCC GAG TTG CCG CCA CAG CAG TTC GCG ACC CTG CTG CGC GAG CTC GGC CGG GAA CGC CGC CTC CAA CTT CAC GAA CCC GTC
    < P   D   M   G   L   Q   R   W   L   L   E   R   G   Q   Q   A   L   E   A   P   F   A   A   E   L   K   V   F   G   D
8086 GGA GAC GAA CCG CTC GAC CTG CTC GTC GCT GAG GAC CTG GGC GCT CAT CGC ACT CCT TCC CGC CGG TTC CCG CCG AGG CGG AGC GAG ACG
    < S   V   F   R   E   V   Q   E   D   S   L   V   Q   A   S   M
8176 GTC GCA CCC GCG CTG ACC GGA CCG GGC GAC GCG CCT CGT CAA GAT TCG CCA GGT TGA ATG GTA GAC AAG CCG CCA CCG TCA GGG ACT AAC
                                                                                                    <   •   P   S   V
8266 GTT TTC CTC AGC ATC GTC CGG GCC ACC GCG AGA GCG CCG CAC CCC CCG CTC CAC CAC CCG CAA CCA TCG GCT CTC CCC GGG TGC GGC GAT
    < N   E   E   A   D   D   P   G   G   R   S   R   R   V   G   R   E   V   V   R   L   W   R   S   E   G   P   A   A   I
8356 GCC GTC GAG CCG GGC GCG GGC CTC CTC CGG CAG CGG CCG GTC GGC CGC CGC CAG CGC CGC CCG GGC CTG GTC CAG CGT GCG GGG GCC GAC
    < G   D   L   R   A   R   A   E   E   P   L   P   R   D   A   A   A   L   A   A   R   A   Q   D   L   T   R   P   G   V
8446 GAC CGT GCT GGT CAC CCC CGG CGC GTC GTA GAC CCA GGC GTG CGC CAG GTC CGG CAG GGA CAG GCC CAG CTC GAC GGC CAC CTT CGC CAA
    < V   T   S   T   V   G   P   A   D   Y   V   W   A   H   A   L   D   P   L   S   L   G   L   E   V   A   V   K   A   L
8536 CCG GCC CAG GGT CCG CCA CAC CGG CTG CCA GTG CGG GCC CGA TGG GGC GTA CCA GGC GGT GAA CCG GGC GTC GCG GGG CGG CTC GCC GTC
    < R   G   L   T   R   W   V   P   Q   W   H   P   G   S   P   A   Y   W   A   T   F   R   A   D   R   P   P   E   G   D
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FIGURE 12E

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8626 GGC GAA CCG GTC GGA GAG CAG ACC CAT CGC CAG CGG GCT GTA GGT GAA CAG GCC GAG GCC GTA CTC CGC GCA CAG CGG CAG CAC GTC CCG
    < A   F   R   D   S   L   L   G   M   A   L   P   S   Y   T   F   L   G   L   G   Y   E   A   C   L   P   L   V   D   R
8716 CTC GAT CTC GCG TTC CAG CAG GTT GTA CGG CGA CTG CTC GGC CAC CAC CGG GGC GGC GCC CCG GGA CTG CGC CGT GCG CAG CAG GTC GAC
    < E   I   E   R   E   L   L   N   Y   P   S   Q   E   A   V   V   P   A   A   G   R   S   Q   A   T   R   L   L   D   V
8806 GAT CCG CCA GCT GGG CAC CGT GCC CAG CCG GGG CTG GTC GGC CAG CTC GTA TGC CGT GGG CAC GGT GGA GGT GCC CAC GTA GCG GAC CTT
    < I   R   W   S   P   V   T   G   L   R   P   Q   D   A   L   E   Y   A   T   P   V   T   S   T   G   V   Y   R   V   K
8896 GCC CGA GCG GAC CAG GTC GTC GAG GGC GGA CAC CGT CTC CTC CAC CGG AGT GTC CGG GTC GTG ACG GTG CAG GTA GAG CAG GTC GAT GTG
    < G   S   R   V   L   D   D   L   A   S   V   T   E   E   V   P   T   D   P   D   H   R   H   L   Y   L   L   D   I   H
8986 GTC GGT ACC CAG CCG GCG CAA CGA CCG CTC GCA CTC CCG CTT CAG GGC GTA CGC CGA GGT GCC CCG GTC GTT CGG TCC CGG GCC GAC CGG
    < D   T   G   L   R   R   L   S   R   E   C   E   R   K   L   A   Y   A   S   T   G   R   D   N   P   G   P   G   V   P
9076 ATT GAA GAT CTT GGT GGC CAG CAG GAC GTC GTC CCG GCA GCT CCG CAC GGC CGC GCC GAC GAT CTC CTC GCT GCG GCC GTC CTG GTA GAC
    < N   F   I   K   T   A   L   L   V   D   D   R   C   S   R   V   A   A   G   V   I   E   E   S   R   G   D   Q   Y   V
9166 GTT GGC CGT GTC GAC GAG GTT GAC TCC CGC TTC GAC GGC CGT GGC GAC GAT CCT GGC GGC CTC CTC CGG CCC GGT CGG GCC GCC GAA GTT
    < N   A   T   D   V   L   N   V   G   A   E   V   A   F   A   V   I   R   A   A   E   E   P   G   T   P   G   G   F   N
9256 GAA CGC CCC CAG GGA CAC CTT GGA CAC CCG CAG TCC ACA CCG GCC CAA CTG TCG GTA CTC CAC GCTGCCCTCCCCTGCGGTGGTGGTCGCCGGCCACCC
    < F   A   G   L   S   V   K   S   V   R   L   G   C   R   G   L   Q   R   Y   E   V
9355 CGTCGTGCGGCCGGTGCTCCCCGGAGCCGGGGAGTGGCCGATCTCGATGGGGGAGCCTAGTACCGCGCGGGTGCCTCGGCCGTGGTACTAGCAGAACTGCTAG AGC ATC CGT CGA
9470 GCC GCC GGG CGG CCG GGC GGC AGC CGG TAC GGT GTG CCT GAA CCC ACC ACG GGC CGG CGC CGG ACG ACC GGT CGA CGA GCG ATC GAG CTG
9560 ATC GGC GGG GAG CGG ATG AGC GAC AAG TAC GGC CGC AGT GCG CTG TGG GAA CGG TAC AAC AGC ACA CAG GTG ACC GAG GAG GCG GCG GAC
                        > M   S   D   K   Y   G   R   S   A   L   W   E   R   Y   N   S   T   Q   V   T   E   E   A   A   D
9650 GAC CTC ACC TCC TTC AAG TCG AGC GAC GTC AAC TAC AAG CTC GCC CTC TGG GAT CCC CGG GTC AGC GGG GTC CGC TAC CTG AAG ACG CTC
    > D   L   T   S   F   K   S   S   D   V   N   Y   K   L   A   L   W   D   P   R   V   S   G   V   R   Y   L   K   T   L
9740 ATC TTC AAC CTG GCC GAG AAC CTG GGC GAG GCG AAC CGG GCC CGG TTG CGC CGG ATC GCC AAC CGG GAC GTC GGC GAC CCC ATC TCC GTC
    > I   F   N   L   A   E   N   L   G   E   A   N   R   A   R   L   R   R   I   A   N   R   D   V   G   D   P   I   S   V
9830 GTC TGG GAC GGC GAC CGG ATC TGC ATG GAC TAT CTC CAG GCG GTG CTG GAG CTG GAG TTC TTC TCC CGC CAC GTG CCA CTG GAC GGC GCG
    > V   W   D   G   D   R   I   C   M   D   Y   L   Q   A   V   L   E   L   E   F   F   S   R   H   V   P   L   D   G   A
9920 ACG GTG CTG GAG ATC GGC GCG GGC TAC GGC CGC ACC TGT CAC GCC GTG CTC TCC AAC CAC GAC GTC GCC GCG TAC CAC GTG GTC GAC CTG
    > T   V   L   E   I   G   A   G   Y   G   R   T   C   H   A   V   L   S   N   H   D   V   A   A   Y   H   V   V   D   L
10010 CCG AAC TCC CTC GCT CTG GCC CGC CGC TAC CTG GGC ACG GTG CTC ACC GCC GAG CAG TTG GCG AGG GTC CAC TTC CAC GGC GTC GGC GAG
    > P   N   S   L   A   L   A   R   R   Y   L   G   T   V   L   T   A   E   Q   L   A   R   V   H   F   H   G   V   G   E
10100 GTG GAC GGG CCG CTG AGC GAG CTG CGC TAC GAC CTC GTG ATC AAC ATC GAC TCG TTC GCG GAG ATG ACG GCG GAG ACG GTG CGC GCG TAC
    > V   D   G   P   L   S   E   L   R   Y   D   L   V   I   N   I   D   S   F   A   E   M   T   A   E   T   V   R   A   Y
10190 CTC GCC TTC GTC GCC ACC AGG GCC CGC CAC CTG TAC GTC AAC AAC CCC GTC GGG AAG TAC CTC GAC AAG AGC CTG GAC GGG CAC TTC CAG
    > L   A   F   V   A   T   R   A   R   H   L   Y   V   N   N   P   V   G   K   Y   L   D   K   S   L   D   G   H   F   Q
10280 GGC GAG GCC GTG GTC AAC CTT GCG CTG AGC ACC GGC CTG CTG CGC GAC GTC ATC GAC ATC CAC GAC AAC CAG GCC GTG CGG CGG CAG TCC
    > G   E   A   V   V   N   L   A   L   S   T   G   L   L   R   D   V   I   D   I   H   D   N   Q   A   V   R   R   Q   S
10370 CGG GCG TTC CTC GAC GCG TAC CGG CCG GGG CCG GGC TGG GCC TGC GTG GCG GAG AGC CGG ACG ATC CCG TGG AGC TAC TAC TGG CAG GCG
    > R   A   F   L   D   A   Y   R   P   G   P   G   W   A   C   V   A   E   S   R   T   I   P   W   S   Y   Y   W   Q   A
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FIGURE 12F

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10460 CTC TAC CGG GCC GGC GAG GCG GCC CCG GCA CCC GGG CGG GAT TGA GGTGACCGGCCGAGCGGGCGAGCCCGCCGACCGGCCCGTCGTCGCCGTCCTCGGCGCCTCC
     > L   Y   R   A   G   E   A   A   P   A   P   G   R   D   •
10566 GGCCTGGTCGGCACCGCT GTG CTG GCC GCG CTC GCC GAC CGG GCG GTC ACC GTC CGG GCC GTC GCC CGC CGG GCT GCC GTG CTG CCC GCC GCG
                       > V   L   A   A   L   A   D   R   A   V   T   V   R   A   V   A   R   R   A   A   V   L   P   A   A
10659 CCG GGC CGC GCG GCG TTT GAG GTG GTA CGG GCC GAC CTG ACC GAC CGG GGA GCC CTG GCG GCG GCG GTA CGC GAC GCG ACG GCC GTG GTC
     > P   G   R   A   A   F   E   V   V   R   A   D   L   T   D   R   G   A   L   A   A   A   V   R   D   A   T   A   V   V
10749 AAC CTC ACC CTG GAC AGT TCC GGC TGG CGG GGC GCC GAC GAC GAC CGC AGC GCG CGG GTC AAC GTC GAG CTG ACC CGG GAA CTC GTC GGG
     > N   L   T   L   D   S   S   G   W   R   G   A   D   D   D   R   S   A   R   V   N   V   E   L   T   R   E   L   V   G
10839 ATG CTC CGC CCC GGG CCG GGC GGC ACG CCC ACC ACA CTG GTC TTC GCC GGC TCC GCC TCC CAG GTG GGC CGG CCG CCC CGG ATC CCG ATC
     > M   L   R   P   G   P   G   G   T   P   T   T   L   V   F   A   G   S   A   S   Q   V   G   R   P   P   R   I   P   I
10929 GAC GGC ACC GAG CCG GAC CAC CCC GCC ACC CCG TAC GAC CGG CAG AAG CAG GCC GCG GAG TCG CTG GTC GTG GCG GCC ACC GGG GCC GGC
     > D   G   T   E   P   D   H   P   A   T   P   Y   D   R   Q   K   Q   A   A   E   S   L   V   V   A   A   T   G   A   G
11019 GTC GTG AAC GGG GTG TCG CTG CGA CTG CCC ACC GTG TTC GGC CCG GTG CCG CCG GGC GCC GGG CCC GAC CGG GGC GTG GTG TCC ACG ATG
     > V   V   N   G   V   S   L   R   L   P   T   V   F   G   P   V   P   P   G   A   G   P   D   R   G   V   V   S   T   M
11109 ATC CGC CGG GCG CTG TCC GGA GCG CCA CTG ACC ATG TGG CAC GAC GGC CGG GTG CAA CGG CAA CTG CTG TAC GTG GCC GAC GCC GCC GCC
     > I   R   R   A   L   S   G   A   P   L   T   M   W   H   D   G   R   V   Q   R   Q   L   L   Y   V   A   D   A   A   A
11199 GCC TTC GTG GCG GCG CTG GAC CAC CCC GGG GCG CTG ACC GGC CGG CAC TGG CCG CTC GGC GAC GGC CGG GGT GAA CGG CTC GGG GAC CTG
     > A   F   V   A   A   L   D   H   P   G   A   L   T   G   R   H   W   P   L   G   D   G   R   G   E   R   L   G   D   L
11289 TTC CGC GCC ATC GCC GCC CTG GTG GCC GAG CGG ACC GGT CGG CCA CCG GTG CCG GTG CTG GCC GTG CCC CCG CCC GAC GAG GCC CGG GTC
     > F   R   A   I   A   A   L   V   A   E   R   T   G   R   P   P   V   P   V   L   A   V   P   P   P   D   E   A   R   V
11379 AGC GAC TTC CAC GAC ATG GTC GTT GAC GCC TCG GCC TTC CAG GCG GTC ACC GGG TGG GCG CCC CGG GTG CCG TTG CGC CTC GCG CTG GAC
     > S   D   F   H   D   M   V   V   D   A   S   A   F   Q   A   V   T   G   W   A   P   R   V   P   L   R   L   A   L   D
11469 CGC ACC GTC GCG GCG CTC GCC CGC GAC GAC AGC GGC CCC GAG GCC CCG GGC GGC GTC GGC CCG ACG CGG GCG GAT CAG GCC CGG
     > R   T   V   A   A   L   A   R   D   D   S   G   P   E   A   P   G   G   V   G   P   T   R   A   D   Q   A   R
11553 AAG CCG GAC TCG ATC TCC AGG CAG GTC CGG TAG TCGGGCAGCAACCCACGGGCGAGCGCCTGGTCGAAGGTGATCGCGGTGCGGTCCCGCTCCGACAGGATCGGTTCGAC
     > K   P   D   S   I   S   R   Q   V   R   •
11663 GTCCTCGGGGATGGGCAGGCCCAGCCCGGGGTCGAGCGCGTCGAGCGCCAGTTCGTTCTCGAAGACGTACTCCTGGGACAGGACGTACGACATGACGGTGTCGTCGGCCAGGGCGACGAAC
11784 ATGTGCGCGACCCCGACCGGCAGGTAGACCGCCTGGAACTCCTCGCTGTCGAGCACCACGCTGTCCCACTTGCCGAACGTCGGTGAGCCCACCCGCACGTCGAGGACCAGGTCGAGCACCC
11905 GGCCGTGCGGGCAGGAGACGAACTTCGCGGTGCCGGGCGGGGTACGGGTGAAGTGCAGCCCCCGCAGCGTCCCCCGGCGGGAGACGCTGTAGCTGGTCTGCCGCACGGGGAACAGCGGGTA
12026 CCCGACCGTGTCCCGGAACAACGAGTCGAGATACGGCGAGAGGAACACCCCCCGGTAGTCCGGGTAGACGGTGGGCGCGAAGGCGTACGCGCCTTCGACGGTCAGCGGGCGGGCGGACACC
12147 GGCGGG
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FIGURE 12G